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(54) Title: SYNTHETIC PEPTIDE BASED IMMUNOGENS FOR THE TREATMENT OF ALLERGY		
(57) Abstract <p>The present invention relates to a method for eliciting the production in healthy mammals, including humans, of high titer antibodies to an effector site in human IgE heavy chain, i.e. a site in the CH4 domain of the ϵ-chain, by the use of compositions of synthetic peptide immunogens in either a radially branching multimeric form (such as branching octameric or hexadecameric peptides) or a linearly arranged monomeric form, to inhibit mast cell activation and reduce allergen-induced IgE production. It also relates to the use of such "optimally" designer, carrier protein free, IgE ϵ-chain related immunogens as key components in a synthetic vaccine to provide an immunotherapy for the treatment of allergy. The subject peptides contain immune stimulator sequences, including a built-in helper T cell epitope tandemly linked in a specific orientation, to aid in stimulating the immune response towards the IgE CH4 domain.</p>		

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SYNTHETIC PEPTIDE BASED IMMUNOGENS
FOR THE TREATMENT OF ALLERGY

CROSS REFERENCE TO RELATED APPLICATION

5 This is a continuation-in-part application of
pending Application Serial No. 08/218,461 filed March 28,
1994 which is a continuation of pending application Serial
No. 08/060,798 filed May 10, 1993 which is a continuation-
in-part of pending application Serial No. 07/847,745,
10 filed March 6, 1992, now abandoned, which was a
continuation-in-part of application Serial No. 07/637,364,
filed January 4, 1991, now abandoned.

FIELD OF THE INVENTION

15 The present invention relates to the use of a
composition of a synthetic peptide, in a linear or
radially branching multimeric form, as an immunogen for
eliciting the production in healthy mammals, including
humans, of high titer antibodies to the effector site on
the CH4 domain of the ϵ -chain of the human IgE heavy
chain, and to the use of the composition as a vaccine to
20 provide an immunotherapy for the treatment of allergy.

BACKGROUND OF THE INVENTION

Immunotherapy for the prevention of IgE-mediated
allergic responses, such as asthma and hay fever, as known
and practiced since early in this century, has been by
25 desensitization or hyposensitization, wherein a gradually
increasing amount of an allergen is given to a patient to
reduce the effects of subsequent exposure to that
allergen⁽¹⁾. Limitations to such an allergen-based
immunotherapy include difficulties in identifying the
30 allergen involved and, if an allergen is identified, the
adverse reactions frequently caused by the use of the
identified allergen⁽²⁾.

Other treatments for the relief of allergies
35 employ drugs to block the cascade of cellular events that

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is responsible for allergic reactions. These drugs include anti-histamines, decongestants, β_2 agonists, and corticosteroids. Anti-histamines, decongestants, and β_2 agonists act on events downstream of IgE in the allergic cascade, making them palliative remedies which address only the allergy symptoms. Preventative treatments must act on cellular events closer to the initiation of IgE-mediated allergic reactions. These palliatives provide relief that is short term and partial. Moreover, the relief of symptoms is frequently accompanied by adverse side effects, e.g. anti-histamines may cause restlessness or drowsiness, and β_2 agonists have sometimes been associated with increased morbidity in asthmatic patients.

Corticosteroids are powerful immunosuppressants and are highly efficacious for the treatment of allergic symptoms. However, they stimulate adverse hormonal activities and may cause an undesirably broad immunosuppression.

To avoid the shortcomings of the known therapeutic drugs, it would be more desirable to prevent allergic responses by selective suppression targeted to IgE. This may be accomplished either by suppressing IgE synthesis, such as is achieved by the inconvenient desensitization method; or by blocking the process by which IgE-allergen complexes stimulate the degranulation of mast cells and basophils with the concomitant release of the chemical mediators of hypersensitivity.

At a more fundamental level, Stanworth et al.⁽³⁻⁷⁾ and others⁽⁸⁻¹³⁾ have used synthetic IgE ϵ -chain peptides and the corresponding antibodies to study the role of cytophilic peptides in cell signaling processes, in an attempt to elucidate the molecular basis for the immunological triggering of mast cells and basophils.

Among the many IgE peptides studied over the past two decades (Table 1), a potential effector site within the Fc CH4 domain of the human ϵ -chain (Lys₄₉₇-

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° Phe₅₀₆, shown in Table 2 by double underlining) was the decapeptide. It was synthesized and used for structure/activity studies⁽³⁾. This IgE CH4 domain-derived decapeptide was found to be capable of activating dose-dependent histamine release from isolated rat peritoneal mast cells in a non-cytolytic manner resembling the IgE-mediated mast cell triggering process⁽⁴⁾. Precise structural requirements for this peptide effector site were deduced through structure-activity studies using multiple synthetic analogues of the ϵ -chain decapeptide^(3,4,5).

Anti-IgE CH4 peptide antibodies derived from immunizations with ϵ chain-related "peptide-carrier protein conjugates" were also used for structure action studies on the degranulation of IgE-sensitized cells, by observing inhibitory activities^(5,11,12).

The feasibility of using a peptide based vaccine to provide immunotherapy to patients with IgE-mediated sensitivities has been suggested by Stanworth et al.^(14,15). He used the previously identified ϵ -chain decapeptide with a sequence of Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe-NH₂⁽³⁾ (SEQ ID NO:1) conjugated to a "carrier protein", such as keyhole limpet hemocyanin (KLH) or the purified protein derivative (PPD) of tuberculin, and found that the "peptide-carrier protein" conjugates elicited decapeptide-specific antibodies. For example, a rabbit anti-peptide serum, selected on the basis of its better-than-average anti-peptide titer, reduced the decapeptide-induced histamine release from rat peritoneal mast cells in a titer-dependent fashion. This inhibitory activity was further confirmed by in vivo tests in a rat passive cutaneous anaphylaxis (PCA) model system. The effect of this rabbit anti-peptide serum on anaphylaxis was assessed, by measurement of the area of blueing and by an estimate of color intensity when given to rats which had been previously sensitized by multiple allergen

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- ° application prior to anaphylactic challenge with the allergen.

In the same study, results obtained in rats using immunogens containing such "decapeptide-protein carrier conjugates" gave preliminary indications of feasibility for their use as a vaccine for the treatment of allergy.

However, this strategy has met with considerable difficulties. The major deficiencies of this prototype "decapeptide-protein carrier conjugate" vaccine include a less-than-optimal immune stimulatory capability and manufacturing difficulties stemming from the poorly defined composition of the carrier protein and the non-uniformity of the conjugation reaction. It has also been found that the resultant antisera raised by such peptide-protein conjugates frequently contain more antibodies directed at the epitopes on the protein carrier, e.g. Keyhole Limpet Hemocyanin (KLH), than to the target-peptide⁽⁵⁾.

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TABLE 1
 IGE HEAVY CHAIN PEPTIDES USED IN STRUCTURE-ACTIVITY STUDIES

Amino Acid Res. Nos. and Peptide Sequence	Domain	Structure-Activity Studies	References
Hu E 497-506 RTKSGFFVF	CH4	Involved in non-antigen receptors in mast cell signalling processes	Stanworth, <u>Mol. Immunol.</u> , 21:1183-1190, 1984(4) Stanworth and Burt, <u>Mol. Immunol.</u> , 23:1231-1235, 1986(5)
Hu E 301-376	CH2/CH3	Blocking of passive sensitization of human mast cells and basophils	Helm et al., <u>PNAS</u> , 86:9465-9469, 1989(13)
Hu E 363-376	CH3	Not essential for binding of the peptide to Fc ϵ -chain receptor I.	ibid.
Hu E 367-376	CH3	Binding to the low affinity IgE receptor (CD23)	Chretien et al., <u>J. Immunol.</u> , 141:3128-3134, 1988(11)
E. coli-derived human FcE fragment	CH2/CH3/CH4	Expression in <i>E. coli</i> and comparison to cell-binding activity of native human IgE myeloma. Recombinant Fc had 20% of native binding activity.	Kenten et al., <u>PNAS</u> 81:2955-2959, 1984(12)
E. coli-derived human FcE fragment	CH2/CH3/CH4	Monomeric form was inactive. The Fc-like dimeric form displayed only % of the cell-binding activity of native IgE.	Coleman et al., <u>Eur. J. Immunol.</u> , 15:966-969, 1985(13)
Rat E 414-428(p129)* 459-472(p124) 491-503(p128) 542-557(p123)	CH3/CH4	Inhibiting binding of rat IgE to mast cells by 20-50% at concentrations between 10^{-4} - 10^{-6} M. *Even the most active peptide(p129) was found 1000-times less active than the active rat IgE.	Burt and Stanworth, <u>Eur. J. Immunol.</u> , 17:437-440, 1987(9)
378-396(p130) 522-535(p122) 560-571(p131)	CH3/CH4	No inhibition	

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Amino Acid Res. Nos. and Peptide Sequence	Domain	Structure-Activity Studies	References
rat ϵ 459-472 (YVFLPPEEEKDKD) 542-547 (HEAKRELRTISK)	CH4	Contribute to the heat-sensitive region of the IgE molecule which is cytophilic for mast cells and basophils.	Stanworth and Burt, <u>Mol. Immunol.</u> , 23:1231-1235, 1986(5)
hu ϵ pentapeptide 330-334 (DSDPR)	CH2	Non-specific inhibition of IgE antibody mediated PK reactions in human.	Hamberger, <u>Science</u> , 189:389-390, 1975(8)
Mouse ϵ peptides	CH2/CH3/CH4	Structure-function relationships defined by sequence directed antibodies	Robertson and Liu., <u>Mol. Immunol.</u> , 25:103-113, 1988(12)
167-180 (P1)	CH2	Anti-p1 displays low binding to IgE.	
207-218 (P2)	CH2/CH3	Hydrophobic and conformational. Anti-p2 does not bind IgE. Inaccessible.	
237-251 (P3)	CH3	Most proximal to IgE-receptor recognition site; anti-p3 showed least IgE binding activity.	
291-305 (P4)	CH3	Anti-p4 stimulated serotonin release.	
338-352 (P5)	CH4	Anti-p5 stimulated serotonin release.	
372-385 (P6)	CH4	Anti-p6 binds best to IgE (in either free or receptor bound forms), however, not effective in crosslinking of IgE-receptor complex.	

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It is known to those of skill in the art, small peptides are poor immunogens. To make small peptides immunogenic, they are usually joined to large carrier proteins by chemical conjugation or by gene fusion. These processes, however, generally produce unpredictable conformational changes in a peptide. Further, the immune response is frequently misdirected to the immunodominant carrier. Consequently, the development of a potent vaccine to provide long-lasting relief from allergies awaits further immunogen design.

In Table 2, the amino acid sequences for the CH2 to CH4 domains of rat IgE ϵ -chain⁽¹⁶⁾ and mouse ϵ -chain⁽¹⁷⁾ are aligned with the amino acid sequence for human ϵ -chain⁽¹⁸⁾ (SEQ ID NOS:2-4) to provide a guide for IgE-related peptide fragments previously reported. It is to be noted that in human IgE ϵ heavy chain, L next to Q at position 252 is not present in the original IgE myeloma ND sequence. Gaps, indicated by dashes, have been introduced to maximize homology. Matches of homologous residue positions are boxed. The positions on the ϵ sequences which have been studied for structural activity (Table 1) are underlined in Table 2. The structurally active IgE CH4 decapeptide sequence in the human IgE CH4 domain is double underlined (SEQ ID NO:1). The amino acid code used in the Table is: A, alanine; R, arginine; N, asparagine; D, aspartic acid; C, cysteine; Q, glutamine; E, glutamic acid; G, glycine; H, histidine; I, isoleucine; L, leucine; K, lysine; M, methionine; F, phenylalanine; P, proline; S, serine; T, threonine; W, tryptophan; Y, tyrosine; V, valine.

Table 2

Table 2

Sequence

Human ε
(SEQ ID
NO:2)
Rat ε
(SEQ ID
NO:3)
House ε
(SEQ ID
NO:4)

224	VCSRDFTPPTVKILQSS -	CDGGGNFPPTIQL (L)	CLVSGYTPGTINITWLED -	GQVMDVDLSTASTTQEGE
249	VRPVTLSLSPWYSIHRC -	PNAFHSTIQL Y	CFIYGHILNDVSVSULMD	DREITDTLAQTVLKEEGK

Human ε
Rat ε
Mouse ε

298	LASTQSQ	LTLSQKHWS	DRITYT	CQVTYQGH	TFQDST	KKCADSNPRGV	SAYLSR	PSPPFDL	FIRKSPITIT
323	NLNI	TQQQW	SESTFT	CKVTSQ	GENYWA	HTRRCSD	DEPRGV	ITYLI	PPSPLDLYENGTPKLT
348	LASTCSKLN	ITEQQW	SESTFT	CRVTSQ	GCDYL	AHTRRCPD	HEPRGA	ITYLI	PPSPLDLYQNGAPKLT

Human ε
Rat ε
Mouse ε

372	CLVLDLAP	SKGT	VNL	TWSRA	SGKP	VNNSTR	KEEKQR	NGTL	TVTSTLPVGT	RDWIEGE	TYQCR	VITHPH			
395	CLVLDL	SEEE	NIT	VTWVR	ERKKS	IGSAS	QRST	KHH	NATTS	ITSILPVD	AKDWIEGE	GYQCR	VDHHPH		
421	CLVVDL	E	SEKN	VN	VTW	NQE	KKTS	VSA	SQVYT	KHHN	NATTS	ITSILPVD	AKDWIEGY	GYQCT	VDPRPD

Table 2 (cont'd)

Human ϵ	LPRALMRSTTK-TSGPRAAPEVYAFATPEWPGSRDKRTLLACLIQNFMPEDISVQWLHNEVQLPDARHS	446	517	542	547
Rat ϵ	FPKPIVRSITK-ALGLRSAPEVYVFLPPE-EEEEKTKRTLTCLIQNFFPE				
Mouse ϵ	FPKPIVRSITLPPQVSQRSAPPEVYVFPPE-EESEDKRTLTCLIQNFFPEDISVQWLGDKGLISNSQHS				
Human ϵ	TTQPRKTKGS--GFFVFSRLEVTRAEM-QEKDEFICRAVHEAASPSQTVQRAVSVPNGK	495	517	542	547
Rat ϵ					
Mouse ϵ	TTTPLKSNQNGFFIFSRLEVAKTLWTQRKQ-FTCQVHEALQKPR				

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OBJECTS OF THE INVENTION

It is an objective of the present invention to employ a group of IgE ϵ -chain based peptide immunogens chemically synthesized in either a radially branching form or a linear T helper epitope containing form, to elicit high titer antibodies to the decapeptide effector site of the CH4 domain of the human ϵ -chain, when introduced to mammals, including humans.

Another objective is to design optimal peptide immunogens, with specific amino acid sequences taken from the human IgE heavy chain CH4 domain (IgE CH4) attached to peptides containing promiscuous human helper T cell epitopes in a specific orientation which, when introduced into mammals, including humans, will stimulate production of high titers of efficacious antibodies to the effector site on human IgE CH4. These antibodies should inhibit mast cell activation, reduce the release of chemical mediators such as histamines that are responsible for allergy symptoms, depress IgE-mediated passive cutaneous anaphylaxis (PCA) reaction, and suppress allergen-induced IgE production by B lymphocytes.

A further objective is to develop an effective IgE ϵ -chain peptide-based vaccine, employing compositions containing such branching multimeric or linear immunogens, to provide immunotherapy for the treatment of allergic reactions.

SUMMARY OF THE INVENTION

According to the present invention, peptide immunogens are made by solid phase synthesis. The peptide immunogens comprise a series of radially branched multimeric peptides containing a ten amino acid IgE CH4 peptide (SEQ ID NO:1), or an immunogenic analog thereof; a series of multimeric branched peptides containing the IgE CH4 peptide (SEQ ID NO:1) or an immunogenic analog thereof together with a helper T-cell epitope (Th epitope); and a

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series of linear monomeric peptides containing the IgE CH4 peptide (SEQ ID NO:1) or an immunogenic analog thereof together with a portion of a helper T-cell epitope (Th epitope). The IgE CH4 peptide is taken from the Fc region of the IgE heavy chain, i.e. ϵ -chain CH4 domain (IgE CH4). Of the three series of peptide immunogens, the linear peptides are preferred. Compositions containing these peptides are used to immunize healthy mammals, e.g. guinea pigs, rats, and humans, to elicit the production of high titer antisera specific for the IgE CH4 effector site (SEQ ID NO:1) and free of irrelevant antibodies.

According to the present invention, vaccines containing the synthetic peptides as the key immunogen may also be prepared with an effective amount of a multimeric-branching peptide or a linear peptide in the presence of a proper adjuvant and/or delivery vehicle. It is expected that such vaccine compositions will elicit a more focused anti-IgE peptide response than those of the peptide-carrier protein conjugates currently used by Stanworth et al.⁽¹⁴⁾, thus providing a better immunotherapy for the treatment of allergy.

DETAILED DESCRIPTION OF THE INVENTION

This invention is directed to the use of a novel group of peptide-based immunogens for the generation of high titer antibodies to an effector site on the CH4 domain of human IgE ϵ heavy chain (SEQ ID NO:1) in healthy mammals, including humans, for the treatment of IgE-mediated allergic diseases.

It is generally accepted that allergy symptoms, the immediate result of IgE-dependent hypersensitivities, are caused by chemical mediators released by mast cells and basophils. The release is triggered when a mast cell or basophil that has been sensitized with surface-bound IgE binds to an allergen for which the surface-bound IgE is specific. The triggering is actuated by the binding of

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the allergen to the Fab' portion of the surface-bound IgE in an antigen-antibody type interaction. The allergen/antibody binding crosslinks the bivalent surface-bound IgE and induces a conformational change in the distal Fc region of IgE, the region of IgE in direct contact with a high affinity Fc receptor on the cell surface. By a mechanism as yet not precisely understood, the conformational change activates the cell-IgE-allergen complex with the resultant release of mediators, including histamine, by the cell. Effector site(s) on IgE are believed to participate in the triggering event. The presence of specific anti-IgE antibodies directed against such "effector sites", through either active or passive immunization, may lead to inhibition of the cell activation process in hosts suffering from allergic reactions by interfering with the interaction between the IgE "effector sites" and the cell surface.

Such interventions through the use of specific anti-IgE antibodies, i.e. a kind of immunotherapy, can be achieved either passively, through prophylactic treatment with specific "site-directed" antibodies to IgE, or, more preferably, actively, by providing the host with a vaccine comprised of site-directed peptide immunogens, to elicit the production by the host of its own site-directed anti-IgE antibodies. It is believed that active immunization will provide a more effective and longer lasting protection.

Among the sites from the Fc region of circulating IgE that have been studied for functional activity, a region on the CH4 domain of the IgE molecule (Lys₄₉₇-Phe₅₀₆) has been identified as a conformational effector involved in the triggering of mast cells and basophils^(3-8,14). See Table 1 and the areas underlined in Table 2. A decapeptide derived from this site with the sequence Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe-NH₂ (SEQ

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ID NO:1) was found to approximate the conformation of this effector site. This is evidenced by the ability of the decapeptide to elicit dose-dependent histamine release from rat mast cells in a manner resembling the immunological triggering process⁽⁴⁾.

5 Stanworth et al.^(14,15) demonstrated the feasibility of providing immunotherapy to patients with IgE-mediated allergic reactions through the use of experimental vaccines by using the IgE CH4 decapeptide (SEQ ID NO:1) coupled to a carrier protein, keyhole limpet hemocyanin (KLH) as an immunogen. Animal immune sera obtained from such immunizations were found by Stanworth et al.^(14,15) to moderately reduce the decapeptide-induced histamine release from rat peritoneal mast cells in a titer-dependent fashion. Inhibitory activity by the immune sera generated was further confirmed by *in vivo* passive cutaneous anaphylaxis (PCA) tests under conditions of multiple allergen application.

10 A major deficiency of the prototype "IgE CH4 peptide" vaccine developed by Stanworth et al is its weak immunogenicity, a problem inherently associated with almost all self-antigens.

15 In the present invention, specific immunogens are provided wherein synthetic immune stimulatory elements are linked to the CH4 decapeptide of IgE (SEQ ID NO:1) in a specific orientation such that potent antibodies directed to this effector site on IgE can be broadly generated in a genetically diverse host population. In turn, these antibodies block the stimulatory action of IgE on mast cells and basophils, thus resulting in an effective treatment to prevent IgE-mediated allergic diseases.

20 The peptide immunogens of the present invention are capable of eliciting antibodies with serological cross-reactivity with the target amino acid sequence of

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the Fc region of IgE (SEQ ID NO:1) while being substantially incapable of mediating non-cytolytic histamine release.

5 The initial dose, e.g. 0.2-2.5 mg; preferably 1 mg, of immunogen is to be administered by injection, preferably intramuscular, followed by repeat (booster) doses. Dosage will depend on the age, weight and general health of the patient as is well known in the therapeutic arts.

10 While there is no particular limitation to the species of mammals suitable for the production of antibodies, it is generally preferred to use mice, rabbits, guinea pigs, pigs, goats, rats or sheep, etc. as the hosts.

15 For active immunization, the term "immunogen" referred to herein relates to synthetic peptides which are capable of inducing antibodies against the IgE CH4 decapeptide (SEQ ID NO:1), which antibodies lead to the suppression of IgE-mediated basophil and mast cell
20 degranulation. The immunogen of this invention included multimeric peptides or its analogs with a branching lysyl core matrix structure.

25 These branched multimeric peptides have the capability of independently eliciting an immune response in a host animal. The analogs of IgE CH4 decapeptide (SEQ ID NO:1) include the synthetic peptide analogs described by Stanworth et al.^(3,4,5), which are incorporated herein by reference. To be suitable, the molecular weight of the immunogen should be higher than 5,000 and preferably be
30 higher than 10,000. The repeating branch unit for the peptide should be equal to or higher than 4.

Bifunctional amino acids such as lysine followed by attachment to an amino acid with a preferably non-charged side chain, such as Gly or Ala, are useful in the
35 making of the core matrix structure. By inserting an

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amino acid in one additional coupling cycle in between two di-Boc-Lysine coupling cycles, the amino acid acts as a spacer in between the peptide branches to allow maximum freedom to attain the conformation necessary for optimal presentation.

The immunogen referred to in the present invention also included linear peptides which contain promiscuous helper T cell epitopes (Th epitopes). These Th epitopes were covalently attached in a defined fashion to the decapeptide effector sequence (SEQ ID NO:1), with or without a spacer, so as to be adjacent to the N terminus of the decapeptide, in order to evoke efficient antibody responses. The immunogen may also be comprised of an immune stimulatory sequence corresponding, for example, to a domain of an invasin protein from the bacteria *Yersinia* spp⁽¹⁹⁾. The invasin domain may also be attached through a spacer to a Th epitope.

The "immunogen" of the present invention minimizes the generation of irrelevant antibodies, thus eliciting a more focused immune response to the "target sequence", i.e., the desired IgE CH4 cross-reactivity (SEQ ID NO:1), without producing undesirable side effects which may complicate the immunotherapy process for the treatment of allergy.

However, when a short target sequence, such as the 10 amino acid IgE CH4 segment Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:1), is used to design a carrier protein-free immunogen, one faces serious challenges. A short peptide antigen is usually a T cell-dependent antigen, i.e. the presence of a T helper epitope is required to render a short "target" peptide immunogenic. The short IgE CH4 decapeptide (SEQ ID NO:1) or an immunogenic analog thereof does not contain a T helper cell epitope. The branched multimeric and linear immunogens comprising the short IgE CH4 decapeptide are

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designed herein to provide for artificially built-in functional helper T-cell epitopes.

The peptides immunogens of this invention are represented by the formula

5 (A)_n-(Th)_m-(B)_o-(IgE CH4 peptide)_p,

wherein

A is an amino acid, α -NH₂, a fatty acid, a derivative of a fatty acid, or an invasin domain;

10 B is an amino acid;

Th is a helper T cell epitope or an immune enhancing analog or segment thereof;

IgE CH4 peptide is Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:1) or an immunogenic analog thereof;

15 n is from 1 to 10;

m is from 1 to 4;

o is from 0 to 10; and

p is from 1 to 3.

20 The peptide immunogens of the present invention comprise from about 20 to about 100 amino acid residues, preferably from about 20 to about 50 amino acid residues and more preferably from about 20 to about 35 amino acid residues.

25 When A is an amino acid, it can be any non-naturally occurring or any naturally occurring amino acid. Non-naturally occurring amino acids include, but are not limited to, β -alanine, ornithine, norleucine, norvaline, hydroxyproline, thyroxine, γ -amino butyric acid, 30 homoserine, citrulline and the like. Naturally-occurring amino acids include alanine, arginine, asparagine, aspartic acid, cysteine, glutamic acid, glutamine, glycine, histidine, isoleucine, leucine, lysine, methionine, phenylalanine, proline, serine, threonine, 35 tryptophan, tyrosine and valine. Moreover, when n is

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greater than one, and two or more of the A groups are amino acids, then each amino acid is independently the same or different.

When A is a fatty acid, such as stearic acid or palmitic acid or a fatty acid derivative, such as a tripalmitoyl cysteine (Pam₃Cys) group, it acts as an adjuvant by enhancing the immunostimulating properties of the Th epitope⁽²⁰⁾. When A is a fatty acid or its derivative it is usually located at the amino terminus of the peptide. Furthermore, when one of A is a fatty acid, there are 2 or 3 additional amino acid A moieties. The fatty acids useful in the invention have a hydrocarbon chain of 8 to 24 carbon atoms which may be saturated or unsaturated.

When A is an invasin domain, it is an immune stimulatory epitope from the invasin protein of a *Yersinia* species. This immune stimulatory property results from the capability of this invasin domain to interact with the $\beta 1$ integrin molecules present on T cells, particularly activated immune or memory T cells. The specific sequence for an invasin domain found to interact with the $\beta 1$ integrins has been described by Brett et al⁽¹⁹⁾. In a preferred embodiment, the invasin domain (Inv) for linkage to a promiscuous Th epitope has the sequence:

Thr-Ala-Lys-Ser-Lys-Lys-Phe-Pro-Ser-Tyr-Thr-Ala-
Thr-Tyr-Gln-Phe (SEQ ID NO: 25)

or is an immune stimulatory analog thereof from the corresponding region in another *Yersinia* species invasin protein. Such analogs may contain substitutions, deletions or insertions to accommodate strain to strain variation, provided that the analogs retain immune stimulatory properties.

In one embodiment, n is 4 and A is α -NH₂, lysine, lysine and lysine in that order. In another embodiment n is 1 and A is α -NH₂. In yet another

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embodiment, n is 4 and A is α -NH₂, an invasin domain (Inv), glycine and glycine in that order.

B comprises naturally occurring or the non-naturally occurring amino acids as described above. Each B may be independently the same or different. When B is lysine, a branched polymer can be formed. For example, if n is 7 and all seven B groups are lysine then a branching K core (K₄K₂K) is formed when the peptide synthesis is conducted without protecting the lysyl side chain ϵ -amino group. Peptides with a K core have eight branch arms, with each branch arm being identical and represented as "(A)_n-(Th)_m-" or "(IgE CH4 peptide with built-in-Th)-". In addition, the amino acids of B can form a flexible hinge, or spacer, to enhance the immune response to the Th epitope and IgE CH4 decapeptide or an analog thereof. Examples of sequences encoding flexible hinges can be found in the immunoglobulin heavy chain hinge region. Flexible hinge sequences are often proline rich. One particularly useful flexible hinge is provided by the sequence Pro-Pro-Xaa-Pro-Xaa-Pro (SEQ ID NO:24), where Xaa is any amino acid, preferably aspartic acid. Immunogenicity can also be improved through the addition of spacer residues (e.g. Gly-Gly) between the promiscuous Th epitope and the IgE CH4 decapeptide or an analog thereof. In addition to physically separating the Th epitope from the B cell epitope (i.e., the IgE CH4 decapeptide site or an analog thereof), the glycine residues can disrupt any artifactual secondary structures created by the joining of the Th epitope with the IgE CH4 decapeptide (SEQ ID NO:1) or an analog thereof and thereby eliminate interference between the T and/or B cell responses. Thus, the conformational separation between the helper cell and the antibody eliciting domains permits more efficient interactions between the presented immunogen and the appropriate Th and B cells.

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Th is a Th epitope comprising natural or non-natural amino acids. A Th epitope may consist of a continuous or discontinuous epitope; not every amino acid of Th is necessarily part of the epitope. Th epitopes, including analogs and segments thereof, to be suitable for the present invention are capable of enhancing or stimulating an immune response to the IgE CH4 decapeptide (SEQ ID NO:1) or an analog thereof. Th epitopes that are immunodominant and promiscuous are highly and broadly reactive in animal and human populations with widely divergent MHC types⁽²¹⁻²³⁾. The Th domain suitable for the present invention has from about 10 to about 50 amino acids and preferably from about 10 to about 30 amino acids. When multiple Th epitopes are present (i.e. $m \geq 2$), then each Th epitope may be independently the same or different.

Th epitope analogs include substitutions, additions, deletions and insertions of from one to about 10 amino acid residues in the Th epitope. Th segments are contiguous portions of a Th epitope that are sufficient to enhance or stimulate an immune response to the IgE CH4 decapeptide (SEQ ID NO:1) or an analog thereof.

Th epitopes of the present invention include hepatitis B surface and core antigen helper T cell epitopes (HB_sTh and HB_cTh), pertussis toxin helper T cell epitopes (PT Th), tetanus toxin helper T cell epitopes (TT Th), measles virus F protein helper T cell epitopes (MV_F Th), *Chlamydia trachomatis* major outer membrane protein helper T cell epitopes (CT Th), diphtheria toxin helper T cell epitopes (DT Th), *Plasmodium falciparum* circumsporozoite helper T cell epitopes (PF Th), *Schistosoma mansoni* triose phosphate isomerase helper T cell epitopes (SM Th), *Escherichia coli* TraT helper T cell epitopes (TraT Th) and immune-enhancing analogs and segments of any of these Th epitopes. Examples of Th

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epitope sequences are provided below:

- HB₁ Th: Phe-Phe-Leu-Leu-Thr-Arg-Ile-Leu-Thr-Ile-Pro-Gln-Ser-Leu-Asp (SEQ ID NO:5)
- 5 PT₁ Th: Lys-Lys-Leu-Arg-Arg-Leu-Leu-Tyr-Met-Ile-Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu-Gln-Tyr-Tyr-Asp-Tyr (SEQ ID NO:6)
- 10 TT₁ Th: Lys-Lys-Gln-Tyr-Ile-Lys-Ala-Asn-Ser-Lys-Phe-Ile-Gly-Ile-Thr-Glu-Leu (SEQ ID NO:7)
- TT₂ Th: Lys-Lys-Phe-Asn-Asn-Phe-Thr-Val-Ser-Phe-Trp-Leu-Arg-Val-Pro-Lys-Val-Ser-Ala-Ser-His-Leu (SEQ ID NO:8)
- 15 PT_{1A} Th: Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu (SEQ ID NO:9)
- 20 TT₂ Th: Tyr-Asp-Pro-Asn-Tyr-Leu-Arg-Thr-Asp-Ser-Asp-Lys-Asp-Arg-Phe-Leu-Gln-Thr-Met-Val-Lys-Leu-Phe-Asn-Arg-Ile-Lys (SEQ ID NO:10)
- PT₂ Th: Gly-Ala-Tyr-Ala-Arg-Cys-Pro-Asn-Gly-Thr-Arg-Ala-Leu-Thr-Val-Ala-Glu-Leu-Arg-Gly-Asn-Ala-Glu-Leu (SEQ ID NO:11)
- 25 MV_{1A} Th: Ser-Glu-Ile-Lys-Gly-Val-Ile-Val-His-Arg-Leu-Glu-Gly (SEQ ID NO:12)
- and
- 30 Leu-Ser-Glu-Ile-Lys-Gly-Val-Ile-Val-His-Arg-Leu-Glu-Gly-Val (SEQ ID NO:61)
- HB₂ Th: Val-Ser-Phe-Gly-Val-Trp-Ile-Arg-Thr-Pro-Pro-Ala-Tyr-Arg-Pro-Pro-Asn-Ala-Pro-Ile-Leu (SEQ ID NO:14)
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- MV_{F2} Th: Gly-Ile-Leu-Glu-Ser-Arg-Gly-Ile-Lys-Ala-Arg-Ile-
Thr-His-Val-Asp-Thr-Glu-Ser-Tyr (SEQ ID NO:26)
- 5 TT₄ Th: Trp-Val-Arg-Asp-Ile-Ile-Asp-Asp-Phe-Thr-Asn-Glu-
Ser-Ser-Gln-Lys-Thr (SEQ ID NO:27)
- TT₅ Th: Asp-Val-Ser-Thr-Ile-Val-Pro-Tyr-Ile-Gly-Pro-Ala-
Leu-Asn-His-Val (SEQ ID NO:28)
- 10 CT Th: Ala-Leu-Asn-Ile-Trp-Asp-Arg-Phe-Asp-Val-Phe-Cys-
Thr-Leu-Gly-Ala-Thr-Thr-Gly-Tyr-Leu-Lys-Gly-Asn-
Ser (SEQ ID NO:29)
- 15 DT₁ Th: Asp-Ser-Glu-Thr-Ala-Asp-Asn-Leu-Glu-Lys-Thr-Val-
Ala-Ala-Leu-Ser-Ile-Leu-Pro-Gly-Ile-Gly-Cys
(SEQ ID NO:30)
- 20 DT₂ Th: Glu-Glu-Ile-Val-Ala-Gln-Ser-Ile-Ala-Leu-Ser-Ser-
Leu-Met-Val-Ala-Gln-Ala-Ile-Pro-Leu-Val-Gly-Glu-
Leu-Val-Asp-Ile-Gly-Phe-Ala-Ala-Thr-Asn-Phe-Val-
Glu-Ser-Cys (SEQ ID NO:31)
- 25 PF Th: Asp-Ile-Glu-Lys-Lys-Ile-Ala-Lys-Met-Glu-Lys-Ala-
Ser-Ser-Val-Phe-Asn-Val-Val-Asn-Ser
(SEQ ID NO:32)
- SM Th: Lys-Trp-Phe-Lys-Thr-Asn-Ala-Pro-Asn-Gly-Val-Asp-
Glu-Lys-Ile-Arg-Ile (SEQ ID NO:33)
- 30 TraT₁ Th: Gly-Leu-Gln-Gly-Lys-Ile-Ala-Asp-Ala-Val-Lys-Ala-
Lys-Gly (SEQ ID NO:34)
- 35 TraT₂ Th: Gly-Leu-Ala-Ala-Gly-Leu-Val-Gly-Met-Ala-Ala-Asp-
Ala-Met-Val-Glu-Asp-Val-Asn (SEQ ID NO:35)

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TraT₃ Th: Ser-Thr-Glu-Thr-Gly-Asn-Gln-His-His-Tyr-Gln-Thr-
Arg-Val-Val-Ser-Asn-Ala-Asn-Lys (SEQ ID NO:36)

5 Preferably, the Th epitope is HB_s Th, PT₁ Th, PT₂ Th, TT₁ Th, TT₃ Th, or MV_{F1} Th.

In the monomeric linear peptides of this invention, as described by the Formula (A)_n-(Th)_m-(B)_o-(IgE CH4 peptide), the Th epitope is covalently attached through spacer B to the N terminus of the IgE CH4
10 decapeptide (SEQ ID NO:1). The IgE CH4 peptide is Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:1), a decapeptide. The IgE CH4 peptide may be replaced by an immunogenic analog. The immunogenic analogs thereof may
15 contain a substitution, addition, deletion, or insertion of from one to about four amino acid residues provided that the analog is capable of eliciting an immune response crossreactive with the IgE CH4 decapeptide (SEQ ID NO:1). The substitutions, additions, and insertions may be made
20 with natural or non-natural amino acids as defined herein. Immunogenic analogs of the IgE CH4 peptide (SEQ NO:1) have been identified by Stanworth et al.^(3,4,5) and are incorporated herein by reference.

Accordingly, preferred peptide immunogens of this invention are monomeric peptides containing IgE CH4
25 decapeptide (SEQ ID NO:1) or an immunogenic analog thereof and Th. More specifically, preferred peptide immunogens are those linear constructs containing IgE CH4 (SEQ ID NO:1) or an immunogenic analog thereof; a spacer (e.g Gly-Gly); a Th epitope selected from the group consisting HB_s,
30 Th, PT₁ Th, PT₂ Th, TT₁ Th, TT₃ Th, and MV_{F1} Th (SEQ ID NOS:5,6,11,7,10,61, respectively); and optionally the Inv domain (SEQ ID NO:25). Preferred peptide immunogen compositions include, for example, Peptide Nos. 19-23 and
35 28 (Tables 5 and 6, SEQ ID NOS:51-55,62).

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The peptide immunogens of this invention may be made by chemical synthesis well known to the ordinarily skilled artisan. See, for example, Grant, ed. Synthetic Peptides⁽²⁴⁾. Hence, peptide immunogens may be synthesized using the automated Merrifield techniques of solid phase synthesis with the α -NH₂ protected by either t-Boc or F-moc chemistry using side chain protected amino acids on, for example, an Applied Biosystems Peptide Synthesizer Model 430A or 431. To synthesize a K core moiety on which to synthesize peptide branches, Di- α, ϵ -(t-Boc) lysine residues are used in place of t-Boc lysine with a 2,4-dichlorobenzyl protecting ϵ -amino group.

When A is a fatty acid, it may be added easily to the N-terminus of the resin bound peptide by the well known carbodiimide method. To add Pam,Cys, the lipoamino acid S-[2,3-Bis(palmitoyloxy)-(2R)-propyl-N-palmitoyl-(R)-cysteine (Pam,Cys) is chemically synthesized. Pam,Cys may then be coupled to the N terminus of a peptide by solid-phase synthesis using Pam,Cys-OH in the final coupling step to link the lipoamino acid to a resin-bound peptide chain.

To improve the solubility of the final coupled lipopeptide product, the solid-phase peptide can be elongated with additional serine and lysine residues at the N-terminus.

After complete assembly of the desired peptide immunogen, the resin is treated according to standard procedures to cleave the peptide from the resin and deblock the functional groups on the amino acid side chains. The free peptide is purified by HPLC and characterized biochemically, for example, by amino acid analysis or by sequencing. Purification and characterization methods for peptides are well known to one of ordinary skill in the art.

Other chemical means to generate linear Th-IgE

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CH4 decapeptide constructs of the invention include the ligation of the haloacetylated and the cysteinyl peptide through the formation of a "thioether" linkage. For example, cysteine can be added to the C terminus of a Th-containing peptide and the thiol group of cysteine is used to form a covalent bond to an electrophilic group such as an N^α chloroacetyl-modified or a maleimide-derivatized α- or ε-NH₂ group of a lysine residue that is attached to the N-terminus of the IgE CH4 decapeptide (ID SEQ NO:1) or an immunogenic analog thereof.

The subject peptides can also be polymerized. Polymerization can be accomplished for example by reaction between glutaraldehyde and the -NH₂ groups of the lysine residues using routine methodology. The linear "A-Th-spacer-IgECH4" peptide constructs (e.g., Peptide Nos. 19-23 and 28, SEQ ID NOS:51-55 and 62) may also be polymerized or co-polymerized by utilization of an additional cysteine added to the N-terminus of the linear "A-Th-spacer-IgECH4" construct. The thiol group of the N-terminal cysteine may be used for the formation of a "thioether" bond with a halochloroacetyl-modified or a maleimide-derivatized α- or ε-NH₂ group of a lysine residue that is attached to the N-terminus of a branched poly-lysyl core molecule (e.g., K₂K, K₄K₂K, K₈K₄K₂K).

Alternatively, the longer linear peptide immunogens may be synthesized by well known recombinant DNA techniques. Any standard manual on DNA technology provides detailed protocols to produce the peptides of the invention. To construct a gene encoding a peptide of this invention, the amino acid sequence is reverse translated into a nucleic acid sequence, and preferably using optimized codon usage for the organism in which the gene will be expressed. Next, a synthetic gene is made, typically by synthesizing overlapping oligonucleotides which encode the peptide and any regulatory elements, if

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necessary. The synthetic gene is inserted in a suitable cloning vector and recombinants are obtained and characterized. The peptide is then expressed under suitable conditions appropriate for the selected expression system and host. The peptide is purified and characterized by standard methods.

The efficacy of the peptide immunogen of the present invention may be established by injecting the immunogen into an animal, and then monitoring the humoral immune response to IgE CH4 decapeptide (SEQ ID NO:1) or an immunogenic analog thereof, as detailed in the Examples. Suitable animals include mice, rats, rabbits, guinea pigs, pigs, goats, sheep, or the like.

Another aspect of this invention provides a vaccine composition comprising an effective amount of one or more of the peptide immunogens of this invention in a pharmaceutically acceptable delivery system. Such vaccine compositions are used for prevention of atopic allergic reactions including allergic rhinitis, those of food allergies, asthma, anaphylaxis, and other IgE-mediated hypersensitive reactions such as virally-induced asthma.

Accordingly, the subject peptide immunogens can be formulated as a vaccine composition using adjuvants, pharmaceutically-acceptable carriers or other ingredients routinely provided in vaccine compositions. Such formulations are readily determined by one of ordinary skill in the art and include formulations for immediate release and/or for sustained release, and for induction of systemic immunity and/or induction of localized mucosal immunity, which may be accomplished by, for example, immunogen entrapment by microparticles. The formulation may also include adjuvants or emulsifiers such as alum, incomplete Freund's adjuvant, liposyn, saponin, squalene, L121, emulsigen and ISA 720 and the like.

The vaccine of the present invention may be

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administered by any convenient route including subcutaneous, oral, intramuscular, or other parenteral or enteral route. It may be administered as a single dose or in multiple doses. Immunization schedules are readily determined by the ordinarily skilled artisan.

The vaccine compositions of the instant invention contain an effective amount of one or more of the synthetic peptide immunogens containing the IgE CH4 decapeptide or its immunogenic analog and a pharmaceutically acceptable carrier. The dosage unit form may be formulated to contain about 0.5 μ g to about 1 mg of each peptide per kg body weight. When delivered in multiple doses, the effective dose may be conveniently divided to contain the appropriate amounts per unit dosage form.

The vaccine compositions of the present invention may be formulated to contain a cocktail of two or more of the subject peptide immunogens to enhance immunoefficacy in a broader population and thus provide a better immune response against IgE CH4 decapeptide. For example, a cocktail of Peptide Nos. 19, 20, 21, 23, and 4 is useful. The composition may also be formulated to comprise lipopeptides to provide a built-in adjuvant. The immune response to synthetic IgE CH4 decapeptide-containing immunogens may also be improved by delivery through entrapment in or on biodegradable microparticles of the type described by O'Hagan et al⁽²⁵⁾. The immunogens can be encapsulated with or without adjuvant, including covalently attached Pam,Cys, and such microparticles may carry an immune stimulatory adjuvant such as Freund's Incomplete Adjuvant or alum. The microparticles function to potentiate immune responses to the immunogen, including localized mucosal immunity. Such localized immunity is especially desirable, for example, for mucosally localized allergic reactions. Vaccine compositions in

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microparticulate form may also be formulated to provide time-controlled release for sustained or periodic responses, for oral administration, and for topical administration⁽²⁵⁻²⁶⁾.

5 Examples of specific peptide immunogens are provided herebelow to illustrate the present invention and are to be used to limit the scope of the invention.

EXAMPLE 1

SYNTHESIS OF OCTAMERIC PEPTIDE IMMUNOGENS

10 The following multimeric peptides were synthesized:

Peptide No. 1

[LysThrLysGlySerGlyPhePheValPheGlyProGlyLysThrLysGlySerGlyPhePheValPheGlyLysMet]₈Lys₄Lys₂Lys, (SEQ ID NO:23)

15 Peptide No. 2

[LysThrLysGlySerGlyPhePheValPheGlyProGlyLysThrLysGlySerGlyPhePheValPheGlyProGlyLysThrLysGlySerGlyPhePheValPheGlyLysMet]₈Lys₄Lys₂Lys, (SEQ ID NO:13)

20 The synthesis of the multimeric peptides proceeds by the limited sequential propagation of a trifunctional amino acid to serve as a low molecular weight matrix core is the basis for the formation of a branching multimeric peptide antigen system. The trifunctional amino acid, Boc-Lys(Boc), or di-(Boc)-Lys is most suitable since both N^α- and N^ε- amino acid groups are available as reactive ends. Thus, sequential propagation of di-(Boc)-Lys will generate 2ⁿ reactive ends.

25 For example, the first coupling of di-(Boc)-Lys onto a solid phase resin will produce two reactive amino ends to bind two peptide chains. Sequential generations of a second, third, and fourth step with di-(Boc)-Lys will therefore generate respectively tetravalent, octavalent, and hexadecavalent ends for binding multimeric peptide chains antigens. Such multimeric peptides are useful as

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immunogens. Branched octameric Peptide Nos. 1 and 2 as described above were synthesized for use as immunogens. The branched antigens contain a small heptalysyl core surrounded by a layer of high density of uniform peptide-antigens around the core matrix. This design differs from the conventional peptide-carrier conjugate antigen which contains a large protein carrier such as PPD or KLH and a small peptide antigen randomly distributed on the surface of the protein carrier in many undefined forms.

The synthesis of the octameric peptide immunogens employs a combination of Boc-amino acid resin-bound benzhydrylamide and tBoc-chemistry. For example, an 8-branched heptalysyl core resin was prepared by coupling di-t-Boc Lys onto an extra low loading of 0.14 mmole/g MBHA (4-methylbenzhydrylamine) resin on a Biosearch 9500 instrument. Two coupling cycles of di-(Boc)-Lys for each was followed by two capping reactions using 0.3 M acetylimidazole in DMF dimethylformamide.

Another two di-(Boc)-Lys couplings were added onto the first di-(NH₂) Lys-resin. The substitution level of synthetic octameric resin was then determined by the ninhydrin test and found to have an appropriate level of free -NH₂ groups, based on the theoretical coupling yield, and was used thereafter for the synthesis of octameric peptide immunogen according to the standard t-Boc procedure.

Acid-labile tert-butyloxycarbonyl (t-Boc) was used for the protection of N- α amino acid. The following functional side-chain protecting groups were used: O-benzyl for Thr, Ser, Glu and Tyr; N^t-tosyl for Arg; BOM, i.e., BOC-N^{im}-Benzyloxymethyl for His, N^ε-dichlorobenzoyloxycarbonyl for Lys; S-4-methylbenzyl- for Cys; O-cyclohexyl for Asp and CHO for Trp.

The successive amino acids of Peptides No. 1 and No. 2 were added from the C- to N- terminus as dictated by

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the sequences of Peptide Nos. 1 and 2 (SEQ ID NOS:23,13). The resultant octameric peptidyl resins for Peptide No. 1 and Peptide No. 2 were cleaved by anhydrous HF at 0°C for 1 hr in the presence of 10% v/v anisole. The released multimeric antigens were extracted with acetic acid, washed twice with ether and lyophilized to dryness. The lyophilized multimeric peptides were used as immunogens.

EXAMPLE 2
ACTIVE IMMUNIZATION WITH BRANCHED OCTAMERIC
PEPTIDE IMMUNOGENS USING CFA AND IFA AS ADJUVANTS

(a) Immunization procedure

Groups of Guinea Pigs (N=3 per group) were immunized with each of the two IgE CH4-related multimeric peptide immunogens (Peptide Nos. 1 and 2) and with Peptide No. 3 (SEQ ID NO:1) conjugated to KLH, according to the following protocol: Each animal was injected subcutaneously with a mixture (200 μ L) of the peptide-based immunogen or conjugate (100 μ g/mL) emulsified with an equal volume of complete Freund's adjuvant (CFA). Subcutaneous injections of the peptide-based immunogen mixed with incomplete Freund's adjuvant (IFA) were repeated at days 21, 42, and 63.

(b) Assay of Guinea Pigs immune sera by measuring their Anti-IgE CH4 related peptide response

Anti-peptide antibody activity is determined by ELISA (enzyme-linked immunosorbent assay) using 96-well flat bottom microtiter plates which were coated with the corresponding immunogen. Aliquots (100 μ L) of a peptide immunogen solution at a concentration of 5 μ g/mL were incubated for 1 hour at 37°C. The plates were blocked by another incubation at 37°C for 1 hour with a 3% gelatin/PBS solution. The blocked plates were then dried and used for the assay. Aliquots (100 μ L) of the test guinea pig sera, starting with a 1:10 dilution in a sample dilution buffer and ten-fold serial dilutions thereafter,

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0 were added to the peptide coated plates. The plates were incubated for 1 hour at 37°C. Normal guinea pig serum was used as a control.

5 The plates were washed six times with 0.05% PBS/Tween® buffer. 100 µL of horseradish peroxidase labelled goat-anti-guinea pig antibody was added at a dilution of 1:1,000 in conjugate dilution buffer (Phosphate buffer containing 0.5M NaCl, and normal goat serum). The plates were incubated for 1 hour at 37°C
10 before being washed as above. Aliquots (100 µL) of o-phenylenediamine substrate solution were then added. The color was allowed to develop for 5-15 minutes before the enzymatic color reaction was stopped by the addition of 50 µL 2N H₂SO₄. The A_{492nm} of the contents of each well was
15 read in a plate reader.

The immunogens, Peptide No. 1 and its closely related derivative Peptide No. 2, both in branching multimeric form, were found to be effective in eliciting antibodies specific to the IgE CH4 target sequence (SEQ ID NO:1) through an ELISA inhibition assay. The results,
20 when compared to a control immunogen, the KLH conjugate of monomeric Peptide No. 3 (IgE CH4 decapeptide SEQ ID NO:1) showed that these two multimeric peptide antigens generated a higher level of antibody titers than the KLH conjugate.
25

The successful results of these immunization experiments indicated the generation of a Th epitope in the multimeric system as a result of insertion of Gly-Lys-Met at the C-terminus of the peptide sequence (see SEQ ID NOS:23 and 13, Peptide Nos. 1 and 2) and indicated the
30 importance of certain orientations for effective presentation to the immune system. Other experiments showed that merely making 8- or even 16-branched IgE peptide immunogens containing the IgE CH4 decapeptide (SEQ ID NO:1) or multiple repeats thereof, in other
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orientations, were not effective in the induction of anti-IgE CH4 responses. In fact, out of a total of 19 branched multimeric constructs, Peptide Nos. 1 and 2 were the only ones to display enhanced immunogenicity. In this respect, the high immunogenicity observed with multimeric Peptide Nos. 1 and 2 required experimentation and was not predictable by one skilled in the art.

In addition, the results obtained suggest that a spacer sequence, i.e., Gly-Pro-Gly, incorporated between the short IgE CH4 segments, is necessary to allow free presentation of the epitopes conferred by the subunit sequence. The insertion of a spacer, i.e., Gly-Lys-Met, at the C-terminus prior to linkage to the branched lysine core resin was also found to be necessary for the immunogenicity of multimeric branched IgE CH4 decapeptide (SEQ ID NO:1) synthetic constructs.

EXAMPLE 3

IMMUNIZATION OF RATS WITH LINEAR IMMUNOGENS (SEQ ID NOS:15-22)

A. Immunogen preparation: Peptide immunogens A-H (Table 3) are synthesized by solid phase synthesis using F-moc chemistry on an Applied Biosystems Peptide Synthesizer Model 430A or 431 according to manufacturer's instructions. After complete assembly of the peptide, the resin is treated according to standard procedures to cleave the peptide from the resin and deprotect the functional groups on amino acid side chains. The structure of the peptide immunogens from the amino terminus to the carboxyl terminus is as follows: Peptide immunogen A is a linear peptide with three domains: 3 lysine residues (3K), the hepatitis B surface antigen helper T cell epitope (HB_sTh epitope) and IgE CH4 peptide. Peptide immunogen A is thus represented as 3K-HB_sTh-IgE CH4 peptide. The actual sequences for Peptide immunogen A and for Peptide immunogens B-H are shown in Table 5 (SEQ

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ID NOS:15-22).

For immunizations at weeks 0, 2 and 5, each peptide immunogen is dissolved and combined with an adjuvant solution (Complete Freund's Adjuvant, Incomplete Freund's Adjuvant, or 0.2% Alum) to result in a final concentration of 0.5 mg/ml. The solution is stored at 4°C until use and vortexed for 3 to 5 min prior to injection. Each rat receives 100 µg per injection.

B. Immunization schedule and serum collection:

10 Sprague-Dawley rats (n=5) are immunized subcutaneously (s.c.). Booster injections are given s.c. at weeks 2 and 5. Blood is collected at weeks 3, 6, 7 and 11.

Blood collection from the middle caudal artery is performed following anesthesia of the rats by intraperitoneal injection of 1 mL of sodium pentobarbital (64.8 mg/mL; Anthony Products Co., Accadia, CA) diluted 1 to 10 in 0.9% NaCl. The tails are kept in 48°C ± 0.5°C water for 2 min and rapidly massaged with paper towels (i.e., milked). Blood is collected immediately into a 5 mL syringe outfitted with a 23 gauge needle. Typically, 2 to 2.5 mL of blood is obtained. The serum is collected by centrifugation for 25 min at 3000 rpm. The serum is aliquoted in 300 µL volumes and stored frozen until used for ELISA assays.

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TABLE 3

Sequences of Peptide Immunogens A-H

	Peptide Immunogen	Amino Acid Sequence
5	A 3K-HB ₅ Th-IgECH4	Lys-Lys-Lys-Phe-Phe-Leu-Leu-Thr-Arg-Ile-Leu-Thr-Ile-Pro-Gln-Ser-Leu-Asp-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:15)
10	B PT ₁ Th-IgECH4	Lys-Lys-Leu-Arg-Arg-Leu-Leu-Tyr-Met-Ile-Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu-Gln-Tyr-Tyr-Asp-Tyr-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:16)
15	C PT _{1A} Th-IgECH4	Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:17)
20	D TT ₁ Th-IgECH4	Lys-Lys-Gln-Tyr-Ile-Lys-Ala-Asn-Ser-Lys-Phe-Ile-Gly-Ile-Thr-Glu-Leu-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:18)
25	E TT ₂ Th-IgECH4	Lys-Lys-Phe-Asn-Asn-Phe-Thr-Val-Ser-Phe-Trp-Leu-Arg-Val-Pro-Lys-Val-Ser-Ala-Ser-His-Leu-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:19)
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5	F TT ₃ Th-IgECH4	Tyr-Asp-Pro-Asn-Tyr-Leu-Arg-Thr-Asp-Ser-Asp-Lys-Asp-Arg-Phe-Leu-Gln-Thr-Met-Val-Lys-Leu-Phe-Asn-Arg-Ile-Lys-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:20)
10	G PT ₂ Th-IgECH4	Gly-Ala-Tyr-Ala-Arg-Cys-Pro-Asn-Gly-Thr-Arg-Ala-Leu-Thr-Val-Ala-Glu-Leu-Arg-Gly-Asn-Ala-Glu-Leu-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:21)
15	H MV _{F1} Th-IgECH4	Ser-Glu-Ile-Lys-Gly-Val-Ile-Val-His-Arg-Leu-Glu-Gly-Val-Leu-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:22)

EXAMPLE 4IMMUNIZATION OF RATS WITH LINEAR
IMMUNOGENS (SEQ ID NOS:37-50)

20 Linear peptide immunogens represented as A-Th-GG-IgE CH4, where A may be either NH₂-, Lys-Lys (2K), Lys-Lys-Lys (3K), or an invasin domain (Inv) (SEQ ID NO:25), Th is a T helper peptide, GG is a Gly-Gly spacer, and IgE CH4 is the target decapeptide (SEQ ID NO:1), are

25 synthesized as described in Example 3. These peptide immunogens are shown in Table 4 as Peptide Immunogens Nos. 4-17 (SEQ ID NOS:37-50). The synthesized and cleaved peptides are used to immunize rats to test for efficacy.

30 Efficacy is evaluated on groups of five rats by the experimental immunization protocol outlined below.

Experimental Design:

Immunogen: Peptide Nos. 4-17 (1 per trial)

Dose: 100 µg per immunization

Route: intramuscular

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Adjuvant: Freund's Complete/Incomplete
Dose Schedule: week 0 (FCA), 3 and 6 weeks (IFA)
Bleed Schedule: weeks 0, 3, 6, 8, 10
Species: Sprague-Dawley rats
Group size: 5
Assay: ELISA for anti-peptide activity, solid-phase immunosorbent is monomeric Peptide No. 3 of the IgE CH4 decapeptide sequence (SEQ ID NO:1).

Blood is collected, processed into serum, and stored prior to titering by ELISA as described in Example 2, with the exception of using horseradish peroxidase-labelled goat anti-rat IgG antibody instead of goat anti-guinea pig IgG as the tracer.

TABLE 4

Sequences of Peptide Immunogens Nos. 4-17

Peptide Immunogen	Amino Acid Sequence
4 TT ₁ Th-GG-IgECH ₄	Lys-Lys-Gln-Tyr-Ile-Lys-Ala-Asn-Ser-Lys-Phe-Ile-Gly-Ile-Thr-Glu-Leu-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:37)
5 TT ₂ Th-GG-IgECH ₄	Lys-Lys-Phe-Asn-Asn-Phe-Thr-Val-Ser-Phe-Trp-Leu-Arg-Val-Pro-Lys-Val-Ser-Ala-Ser-His-Leu-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:38)
6 PT _{1A} Th-GG-IgECH ₄	Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:39)

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- 7 MV_{F2}Th-GG-IgECH₄ Gly-Ile-Leu-Glu-Ser-Arg-Gly-Ile-Lys-Ala-Arg-Ile-Thr-His-Val-Asp-Thr-Glu-Ser-Tyr-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:40)
- 5 8 TT₄Th-GG-IgECH₄ Trp-Val-Arg-Asp-Ile-Ile-Asp-Asp-Phe-Thr-Asn-Glu-Ser-Ser-Gln-Lys-Thr-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:41)
- 10 9 TT₅Th-GG-IgECH₄ Asp-Val-Ser-Thr-Ile-Val-Pro-Tyr-Ile-Gly-Pro-Ala-Leu-Asn-His-Val-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:42)
- 15 10 CTTh-GG-IgECH₄ Ala-Leu-Asn-Ile-Trp-Asp-Arg-Phe-Asp-Val-Phe-Cys-Thr-Leu-Gly-Ala-Thr-Thr-Gly-Tyr-Leu-Lys-Gly-Asn-Ser-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:43)
- 20 11 DT₁Th-GG-IgECH₄ Asp-Ser-Glu-Thr-Ala-Asp-Asn-Leu-Glu-Lys-Thr-Val-Ala-Ala-Leu-Ser-Ile-Leu-Pro-Gly-Ile-Gly-Cys-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:44)
- 25 12 DT₂Th-Gg-IgECH₄ Glu-Glu-Ile-Val-Ala-Gln-Ser-Ile-Ala-Leu-Ser-Ser-Leu-Met-Val-Ala-Gln-Ala-Ile-Pro-Leu-Val-Gly-Glu-Leu-Val-Asp-Ile-Gly-Phe-Ala-Ala-Thr-Asn-Phe-Val-Glu-Ser-Cys-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val- (SEQ ID NO:45)
- 30 13 PFTh-GG-IgECH₄ Asp-Ile-Glu-Lys-Lys-Ile-Ala-Lys-Met-Glu-Lys-Ala-Ser-Ser-Val-Phe-Asn-Val-Val-Asn-Ser-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:46)
- 35 14 SMTh-GG-IgECH₄ Lys-Trp-Phe-Lys-Thr-Asn-Ala-Pro-Asn-Gly-Val-Asp-Glu-Lys-Ile-Arg-Ile-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:47)

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°	15	TraT ₁ Th-GG-IgECH ₄	Gly-Leu-Gln-Gly-Lys-Ile-Ala-Asp-Ala-Val-Lys-Ala-Lys-Gly-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:48)
5	16	TraT ₂ Th-GG-IgECH ₄	Gly-Leu-Ala-Ala-Gly-Leu-Val-Gly-Met-Ala-Ala-Asp-Ala-Met-Val-Glu-Asp-Val-Asn-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:49)
10	17	TraT ₃ Th-GG-IgECH ₄	Ser-Thr-Glu-Thr-Gly-Asn-Gln-His-His-Tyr-Gln-Thr-Arg-Val-Val-Ser-Asn-Ala-Asn-Lys-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:50)

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EXAMPLE 5IMMUNIZATION OF RATS WITH LINEAR
IMMUNOGENS (SEQ ID NOS:51-56,62)
AND LINEAR IMMUNOGENS OF REVERSE POLARITY(SEQ ID NOS:57-60)

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Peptide immunogens Nos. 18-23 (ID SEQ ID NOS:51-56) as shown in Table 5, were synthesized as described in Example 3. The formula for peptide immunogens Nos. 18-23 may be represented as A-Th-GG-IgECH4, wherein A is either the N terminus, Lys-Lys (2K), Lys-Lys-Lys (3K), or the
10 invasin domain (Inv) (SEQ ID NO:25) separated from the Th sequence by a spacer GG; Th is selected from the group consisting of HB_s Th, PT₁ Th, PT₂ Th, MV_{F1} Th, or TT₃ Th; GG is a Gly-Gly spacer; and IgECH4 is the IgE CH4 decapeptide
15 (SEQ ID NO:1).

Peptide immunogens with SEQ ID NOS:57-60, also shown in Table 5, as Peptide Nos. 24-27, were synthesized in an identical fashion to the Peptide Nos. 18-23. These peptides may be represented as IgECH4-GG-Th. These
20 peptides are equivalent to Peptide Nos. 19,20,21,23 (Table 5) in terms of IgECH4 decapeptide, spacer, and Th sequences except that the decapeptide/Th polarity was reversed, i.e., the IgE CH4 decapeptide (SEQ ID NO:1) was on the N terminus while Th was located on the C terminus.

25 These peptide immunogens were used to immunize rats as described in the experimental protocol below, for comparison and demonstration of efficacy.

Experimental Design:

Immunogen: Peptide Nos. 18-28 (1 per group)
30 (SEQ ID NOS:51-60 and 62)

Dose: 100 µg per immunization

Route: intramuscular

Adjuvant: Freund's Complete/Incomplete for
Peptide Nos. 18-27, 0.4% Alum for

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Peptide No. 28

Dose Schedule: week 0 (FCA), 3 and 6 weeks (IFA) for
Peptide Nos. 8-27, Alum for Peptide
No. 28 on weeks 0, 3, and 6

5 Bleed Schedule: weeks 0, 3, 6, 8, 10

Species: Sprague-Dawley rats

Group size: 5 for Peptide Nos. 27-28, 4 for
Peptide No. 28

10 Assay: ELISA for anti-peptide
activity, solid-phase substrate is
Peptide No. 3
(SEQ ID NO:1).

15 Blood was collected, processed into serum, and stored
prior to titering by ELISA as described in Example 2 with
the exception of substituting horseradish peroxidase-
labelled goat anti-rat IgG antibody for anti-guinea pig
IgG as the tracer. All sera were assayed by anti-peptide
ELISA and those samples which gave A_{492nm} values of ≥ 0.2 at
a 1:100 dilution were recorded as seropositive.

20 The immunopotencies of Peptide immunogens Nos.
18-28 (SEQ ID NOS:51-60, and 62) were evaluated by the
anti-peptide ELISA and are shown in Table 6 as the number
of rats in each group of 4 or 5 that converted to
seropositive reactivity for IgE CH4 Peptide No. 3 on weeks
25 6 and 8 (i.e., $A_{492nm} \geq 0.2$ at a 1:100 dilution), in
response to the experimental immunizations.

30 The peptide immunogens of this Example of
polarity Th-GG-IgECH4 (Peptide Nos. 18-23 and 28, SEQ ID
NOS:51-56 and 62) showed significant efficacy for the
induction of antibodies to the IgE CH4 decapeptide
(Peptide No. 3, SEQ ID NO:1). All 6 groups of rats
immunized with the peptide immunogens of this polarity
(Peptide Nos. 18-23, 28) showed significant conversion to
seropositivity compared to the control. Prevalences of

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seroconversion for the groups varied from 1/5 to 5/5 by week 6 and seroconversion prevalences continued to increase between weeks 6 and 8 in response to the third dose of immunogens. Peptide immunogen No. 18 containing the HB_s Th peptide sequence, Peptide immunogen No. 19 with the MV_{F1} Th peptide and Peptide No. 28 containing the PT₁Th peptide sequence were the most effective, with seroconversion prevalences of 4/5, 5/5 and 4/4, respectively, by week 8. Comparison of the immunogenicities of Peptide immunogens Nos. 21 and 22 (SEQ ID NOS:54,55) demonstrates that the Inv domain peptide provided significant improvement by week 8 to the immune stimulatory capability of the PT₂ Th-containing peptide (Table 6).

In contrast, the analogous peptide immunogens with reversed Th polarity (Peptide immunogens Nos. 24-27, SEQ ID NOS:57-60) failed to display significant immunopotency for the seroconversion of rats. This poor immunopotency shows that a Th-GG-IgECH₄ amino to carboxyl terminus polarity is critical to the immunogenicity of the linear peptide immunogens of the invention. A determination of efficacy for one orientation of target peptide and Th over the other was not predictable by one skilled in the art and is unexpected.

TABLE 5

Sequences of Peptide Immunogens Nos. 18-28

Peptide Immunogen	Amino Acid Sequence
18 3K-HB _s Th-GG-IgECH ₄	Phe-Phe-Leu-Leu-Thr-Arg-Ile-Leu-Thr-Ile-Pro-Gln-Ser-Leu-Asp-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:51)

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°	19 MV _{P1} Th-GG-IgECH ₄	Leu-Ser-Glu-Ile-Lys-Gly-Val-Ile-Val-His-Arg-Leu-Glu-Gly-Val-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:52)
5	20 PT ₁ Th-GG-IgECH ₄	Lys-Lys-Leu-Arg-Arg-Leu-Leu-Tyr-Met-Ile-Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu-Gln-Tyr-Tyr-Asp-Tyr-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:53)
10	21 PT ₂ Th-GG-IgECH ₄	Gly-Ala-Tyr-Ala-Arg-Cys-Pro-Asn-Gly-Thr-Arg-Ala-Leu-Thr-Val-Ala-Glu-Leu-Arg-Gly-Asn-Ala-Glu-Leu-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:54)
15	22 Inv-GG-PT ₂ Th-GG-IgECH ₄	Thr-Ala-Lys-Ser-Lys-Lys-Phe-Pro-Ser-Tyr-Thr-Ala-Thr-Tyr-Gln-Phe-Gly-Gly-Gly-Ala-Tyr-Ala-Arg-Cys-Pro-Asn-Gly-Thr-Arg-Ala-Leu-Thr-Val-Ala-Glu-Leu-Arg-Gly-Asn-Ala-Glu-Leu-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:55)
20	23 TT ₃ Th-GG-IgECH ₄	Tyr-Asp-Pro-Asn-Tyr-Leu-Arg-Thr-Asp-Ser-Asp-Lys-Asp-Arg-Phe-Leu-Gln-Thr-Met-Val-Lys-Leu-Phe-Asn-Asp-Arg-Phe-Leu-Gln-Thr-Met-Val-Lys-Leu-Phe-Asn-Arg-Ile-Lys-Gly-Gly-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:56)
25	24 IgECH ₄ -GG-MV _{P1} Th	Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe-Gly-Gly-Leu-Ser-Glu-Ile-Lys-Gly-Val-Ile-Val-His-Arg-Leu-Glu-Gly-Val (SEQ ID NO:57)
30	25 IgECH ₄ -GG-PT ₁ Th	Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe-Gly-Gly-Lys-Lys-Leu-Arg-Arg-Leu-Leu-Tyr-Met-Ile-Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-His-Lys-Glu-Glu-Gln-Tyr-Tyr-Asp-Tyr (SEQ ID NO:58)

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°	26	IgECH ₄ -GG-PT ₂ Th	Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe-Gly-Gly-Gly-Ala-Tyr-Ala-Arg-Cys-Pro-Asn-Glu-Thr-Arg-Ala-Leu-Thr-Val-Ala-Glu-Leu-Arg-Gly-Asn-Ala-Glu-Leu (SEQ ID NO:59)
5	27	IgECH ₄ -GG-TT ₃ Th	Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe-Gly-Gly-Tyr-Asp-Pro-Asn-Tyr-Leu-Arg-Thr-Asp-Ser-Asp-Lys-Asp-Arg-Phe-Leu-Gln-Thr-Met-Val-Lys-Leu-Phe-Asn-Asp-Arg-Phe-Leu-Gln-Thr-Met-Val-Lys-Leu-Phe-Asn-Arg-Ile-Lys (SEQ ID NO:60)
10	28	PT ₁ Th-IgECH ₄	Lys-Lys-Leu-Arg-Arg-Leu-Leu-Tyr-Met-Ile-Tyr-Met-Ser-Gly-Leu-Ala-Val-Arg-Val-His-Val-Ser-Lys-Glu-Glu-Gln-Tyr-Tyr-Asp-Tyr-Lys-Thr-Lys-Gly-Ser-Gly-Phe-Phe-Val-Phe (SEQ ID NO:62)

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TABLE 6

5	Peptide Immunogen	Animals Seroconverted/group*	
		Week 6	Week 8
10	18 3K-HB ₉ Th-GG-IgECH ₄ (SEQ ID NO:51)	4	4
	19 MV _{F1} Th-GG-IgECH ₄ (SEQ ID NO:52)	5	5
	20 PT ₁ Th-GG-IgECH ₄ (SEQ ID NO:53)	2	3
	21 PT ₂ Th-GG-IgECH ₄ (SEQ ID NO:54)	1	1
15	22 Inv-GG-PT ₂ -GG-IgECH ₄ (SEQ ID NO:55)	1	3
20	23 TT ₃ Th-GG-IgECH ₄ (SEQ ID NO:56)	3	3
	24 IgECH ₄ -GG-MV _{F1} Th (SEQ ID NO:57)	0	0
	25 IgECH ₄ -GG-PT ₁ Th (SEQ ID NO:58)	1	1
	26 IgECH ₄ -GG-PT ₂ Th (SEQ ID NO:59)	0	0
25	27 IgECH ₄ -GG-TT ₃ Th (SEQ ID NO:60)	0	0
30	28 PT ₁ Th-IgECH ₄ (SEQ ID NO:62)	4	4
	Control Immunization	0	0
	(No peptide)		

*5 animals per group for Peptide Nos. 18-27, 4 animals for Peptide No. 28

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EXAMPLE 6COCKTAIL OF LINEAR IMMUNOGENS
FURTHER BROADENS THE RESPONSIVE POPULATION

Establishing the relative efficacies of the many
5 different linear constructs containing IgE CH4
decapeptide and Th (Examples 3-5) permits selection of
useful peptide immunogens to formulate a cocktail vaccine
composition. Individual Th-GG-IgECH4 constructs carrying
immunodominant promiscuous Th peptides derived from
10 measles virus F protein, tetanus toxin and pertussis toxin
(Peptide Nos. 19-23) were proven by the study of Example 5
to be efficacious in eliciting antibody responses to the
IgECH4 decapeptide (SEQ ID NO:1). A formulation
containing a mixture of these linear peptides may provide
15 a desired maximum immunogenicity in a genetically diverse
population.

The immunopotency of such a composition
formulated to contain a mixture of synthetic peptides with
the preferred "A-Th-GG-IgECH4" polarity, Peptide
20 immunogens Nos. 19, 20, 21, 23 (Table 5) and Peptide
immunogen No. 4 (Table 4, Example 4) were evaluated in
rats by the protocol described in Example 5. Each animal
in a group of 5 rats were immunized with 100 μ g doses of
an equimolar formulation of the 5 peptides, i.e. 20 μ g of
25 each peptide. The number of rats that converted to
seropositive reactivity by weeks 5 and 8 were 5 out of 5
(i.e., 100%) at both time intervals.

The results demonstrate that a vaccine
comprising a cocktail of the peptide immunogens of the
30 present invention provides improved immunogenicity. It
also indicates the potential for this mixture, and of like
cocktails composed of individually efficacious peptides,
to induce immunotherapeutic antibody responses in the
genetically diverse human population.

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EXAMPLE 7IMMUNIZATIONS WITH COCKTAILS OF
EFFICACIOUS LINEAR IMMUNOGENS

Establishing the relative efficacies of the many
5 different linear constructs containing IgE CH4
decapeptide and Th (Examples 3-5) permits selection of
useful peptides for a cocktail of immunogens. Individual
constructs carrying a Gly-Gly spacer and promiscuous Th
peptides derived from measles virus F protein, hepatitis B
10 surface antigen, tetanus toxin and pertussis toxin in the
immunogen cocktail are demonstrated to be efficacious
(Table 6). A mixture of these linear peptide immunogens
with specific polarity with proven efficacy may thus
provide maximum immunogenicity in a genetically diverse
15 population. The protocol below has been designed to
demonstrate efficacy for compositions of the invention
formulated as mixtures of synthetic peptide immunogens
containing preferred "A-Th-GG-IgECH4" constructs.

Experimental Design:

20 Immunogens: (1) Cocktail 1: Peptide Nos. 18, 19, 20
(2) Cocktail 2: Peptide Nos. 18, 19, 22
(3) Positive Control- KLH conjugate of
Peptide 3 (One immunogen per group
of rats)

25 Dose: Molar equivalents of each synthetic
peptide or IgE CH4 equivalent, to
equal either 100 μ g or 33.3 μ g of
peptide per immunization

Route: intramuscular

30 Adjuvants: (1) Freund's Complete/Incomplete
(2) 0.4% Alum (Aluminum hydroxide)
(One of either adjuvant per
immunogen per group)

Dose Schedule: week 0, 2 and 4 weeks

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(CFA/IFA groups receive CFA week 0, IFA weeks 2 and 4. Alum groups receive Alum formulations for all 3 doses)

5 Bleed Schedule: weeks 0, 3, 6 and 8
 Species: Sprague-Dawley rats/group
 Group size: 5, 6 groups
 Assay: ELISA for anti-peptide activity,
 solid-phase immunosorbent is Peptide
10 No. 3 (SEQ ID NO:1).

Blood is collected, processed into serum, and stored prior to titering by ELISA as described in Example 5.

15 This experiment is designed to demonstrate improved performance of the immunogens of the present invention as compared to the known immunogens of the prior art ^(14,15). The results are useful for the evaluation of two mixtures of efficacious peptide immunogens, each
20 containing three Th peptides, demonstrate the usefulness of the immune stimulatory Inv domain (cocktail 2 contains Inv, cocktail 1 does not), and the efficacy of the adjuvant, Alum, in a vaccine composition of the invention.

EXAMPLE 8

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CLINICAL TRIAL USING COCKTAILS OF IMMUNOGENS

Establishing the relative efficacies of the many different constructs containing IgE CH4 decapeptide and Th (Examples 3-5) permits selection of representative peptides for a cocktail of immunogens. Individual
30 constructs carrying a Gly-Gly spacer and Th peptide sequences from measles virus F, hepatitis B surface antigen, tetanus toxin and pertussis toxin in the immunogen cocktail are of demonstrated efficacy (Table 6) and are promiscuous for multiple human HLA DR antigens, so

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as to provide maximum immunogenicity in a genetically diverse human population. Moreover, because these Th peptides are derived from children's vaccines, childhood vaccinations are a potential source of Th memory in an immunized human population. Thus, children's vaccines have the potential to afford enhanced immunopotency to anti-allergy vaccines comprised of mixtures of such Th peptides. The clinical protocol below has been designed to demonstrate efficacy for compositions of the invention formulated as a mixture of such linear "A-Th-Spacer-IgE Ch4 decapeptide" peptide immunogens, in a widely acceptable adjuvant, Alum.

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Experimental Design:

Subjects: Hay fever patients
Season & Duration: Hay fever seasons, 8 weeks
Groups: 4 groups, 1 group/immunogen/dose
N=15 per group, 12 receive immunogen, 3 receive placebo
Immunogen: Cocktail 1: Peptide Nos. 18, 19, 20, 23
Adjuvant: 0.2% Alum
Dose: Molar equivalents of each synthetic peptide to equal 500 μ g or 125 μ g of peptide per dose
Route: intramuscular
Dose Schedule: week 0, and 4 weeks
Evaluation schedule: weeks 0, 4, and 6
Blood is collected, processed into serum, and stored prior to titering by ELISA as described in Example 5.
Efficacy and safety of the vaccine composition "cocktail 1" are evaluated serologically, by skin reaction tests, the rate of patient usage of hay fever medication, physical examination of patients for allergic symptoms and adverse reactions, and interviewing the patients to obtain their subjective assessments of the effect of using the

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products. Serological evaluations include the
aforementioned ELISA for antipeptide titer, and a standard
automated spectrofluorimetric assay to determine reduction
in histamine levels⁽¹⁵⁾ as well as to ascertain that the
5 products do not trigger histamine release. The skin test
is an intradermal test in which a standardized solution of
allergens is injected into the upper layers of the skin.
Reactions to the allergens are quantitated by determining
the area of the typical "wheal and flare" produced in
10 response to the allergens. The expected results include
significant improvement in allergic symptoms at the
endpoint of the study, and no evidence of histamine
release triggered by the vaccine composition of the
invention.

15 This experiment is designed to demonstrate the
clinical efficacy of the invention. The results provide
an evaluation of a mixture of "A-Th-Spacer-IgE CH4
decapeptide" immunogens containing four Th peptide
sequences formulated with a pharmaceutically acceptable
20 adjuvant, Alum.

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EXAMPLE 9IN VITRO ASSAY DEMONSTRATES EFFICACY OF
IgE CH4 DECAPEPTIDE-SPECIFIC ANTIBODIES

5 Passively-sensitized human basophils are used in a well-known histamine-release assay for an in vitro evaluation of antibodies induced by immunizations with IgE CH4 decapeptide immunogens. Human basophils are prepared from the venous blood of volunteers and then passively
10 sensitized with IgE specific for benzylpenicilloyl-human serum albumin conjugate (BPO-HSA) that is prepared from the blood of donors hyperimmunoglobulemic for BPO-HSA-specific IgE. Histamine release by the sensitized basophils is affected by the addition of either BPO-HSA or
15 IgE CH4 Peptide No. 3 (SEQ ID NO:1). Prior to the addition of the agents to induce histamine release, the basophils are combined with serial dilutions of antiserum to IgE CH4 decapeptide (SEQ ID NO:1) or pre-immune control serum. Samples are analyzed for histamine release by the
20 automated fluorescence technique. The percentage of histamine release is calculated from the ratio of sample to total basophil histamine content after spontaneous release is subtracted from both⁽²⁷⁾. The capacity of the experimental antiserum to inhibit histamine release is
25 demonstration of in vitro efficacy.

The ability of the IgE CH4 Peptide No. 3 (SEQ ID NO:1) to induce histamine release in a concentration-dependent manner was demonstrated by this assay. The results, presented in Table 7, showed that the IgE CH4 Peptide No.
30 3 (SEQ ID NO:1) induced histamine release by human basophils and served to validate the relevance of SEQ ID NO:1 and corresponding antibodies for the human allergic response.

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TABLE 7

	Inducer	% Net Histamine Release*
5	Peptide No. 3	
	150 µg/mL (1.3×10^{-4} M)	30%
	60 µg/mL (7×10^{-5} M)	13
	6 µg/mL (7×10^{-6} M)	2
10	BPO-HSA	
	0.1 µg/mL	63%

* Corrected by subtraction of spontaneous histamine release, 9%

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SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANTS: United Biomedical, Inc. & WANG, Chang Yi
- 5 (ii) TITLE OF INVENTION: SYNTHETIC PEPTIDE BASED
IMMUNOGENS FOR THE TREATMENT OF ALLERGY
- (iii) NUMBER OF SEQUENCES: 62
- (iv) CORRESPONDENCE ADDRESS:
10 (A) ADDRESSEE: Maria C.H. Lin
(B) STREET: 345 Park Avenue
(C) CITY: New York
(D) STATE: NY
(E) COUNTRY: USA
(F) ZIP: 10154
- (v) COMPUTER READABLE FORM:
15 (A) MEDIUM TYPE: Floppy disk
(B) COMPUTER: IBM PC compatible
(C) OPERATING SYSTEM: PC-DOS/MS-DOS
(D) SOFTWARE: WordPerfect 5.1
- (vi) CURRENT APPLICATION DATA:
20 (A) APPLICATION NUMBER:
(B) FILING DATE: 24-MAR-1995
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/328,912
(B) FILING DATE: 25-OCT-1994
- (vii) PRIOR APPLICATION DATA:
25 (A) APPLICATION NUMBER: US 08/218,461
(B) FILING DATE: 28-MAR-1994
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 08/060,798
(B) FILING DATE: 10-MAY-1993
- (vii) PRIOR APPLICATION DATA:
30 (A) APPLICATION NUMBER: US 07/847,745
(B) FILING DATE: 06-MAR-1992
- (vii) PRIOR APPLICATION DATA:
(A) APPLICATION NUMBER: US 07/637,364
(B) FILING DATE: 04-JAN-1991

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- ° (viii) ATTORNEY/AGENT INFORMATION:
 (A) NAME: Maria C.H. Lin
 (B) REGISTRATION NUMBER: 29,323
 (C) REFERENCE/DOCKET NUMBER: 1151-4061US4

- (ix) TELECOMMUNICATION INFORMATION:
 (A) TELEPHONE: 212-758-4800
 (B) TELEFAX: 212-751-6849

5

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 10
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: linear
- (ii) MOLECULE TYPE: peptide
- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Stanworth et al.
 (B) TITLE: The Role Of Non-Antigen Receptors
 In Mast Cell Signalling Processes
 (C) JOURNAL: Molecular Immunology
 (D) VOLUME: 21
 (E) ISSUE: 12
 (F) PAGES: 1183-1190
 (G) DATE: 1984
 (J) PUBLICATION DATE:
 (K) RELEVANT RESIDUES: 497 to 506
- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:
- | | | | | | | | | | |
|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Lys | Thr | Lys | Gly | Ser | Gly | Phe | Phe | Val | Phe |
| 1 | | | | 5 | | | | | 10 |

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(3) INFORMATION FOR SEQ ID NO:2:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 325
 (B) TYPE: amino acids
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: Unknown

30

- (ii) MOLECULE TYPE: Polypeptide ϵ -chain of human IgE

- (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Dorrington and Bennich
 (B) TITLE:
 (C) JOURNAL: Immunology Review
 (D) VOLUME: 41

35

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(E) ISSUE:
 (F) PAGES: 3-25
 (G) DATE: 1978

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:2:

	Val	Cys	Ser	Arg	Asp	Phe	Thr	Pro	Pro	Thr	Val	Lys	Ile	Leu	Gln	
					5					10					15	
5	Ser	Ser	Cys	Asp	Gly	Gly	Gly	His	Phe	Pro	Pro	Thr	Ile	Gln	Leu	
					20					25					30	
	Leu	Cys	Leu	Val	Ser	Gly	Tyr	Thr	Pro	Gly	Thr	Ile	Asn	Ile	Thr	
					35					40					45	
	Trp	Leu	Glu	Asp	Gly	Gln	Val	Met	Asp	Val	Asp	Leu	Ser	Thr	Ala	
					50					55					60	
	Ser	Thr	Thr	Gln	Glu	Gly	Glu	Leu	Ala	Ser	Thr	Gln	Ser	Gln	Leu	
10					65					70					75	
	Thr	Leu	Ser	Gln	Lys	His	Trp	Leu	Ser	Asp	Arg	Thr	Tyr	Thr	Cys	
					80					85					90	
	Gln	Val	Thr	Tyr	Gln	Gly	His	Thr	Phe	Gln	Asp	Ser	Thr	Lys	Lys	
					95					100					105	
	Cys	Ala	Asp	Ser	Asn	Pro	Arg	Gly	Val	Ser	Ala	Tyr	Leu	Ser	Arg	
					110					115					120	
15	Pro	Ser	Pro	Phe	Asp	Leu	Phe	Ile	Arg	Lys	Ser	Pro	Thr	Ile	Thr	
					125					130					135	
	Cys	Leu	Val	Leu	Asp	Leu	Ala	Pro	Ser	Lys	Gly	Thr	Val	Asn	Leu	
					140					145					150	
	Thr	Trp	Ser	Arg	Ala	Ser	Gly	Lys	Pro	Val	Asn	Asn	Ser	Thr	Arg	
					155					160					165	
	Lys	Glu	Glu	Lys	Gln	Arg	Asn	Gly	Thr	Leu	Thr	Val	Thr	Ser	Thr	
					170					175					180	
20	Leu	Pro	Val	Gly	Thr	Arg	Asp	Trp	Ile	Glu	Gly	Glu	Thr	Tyr	Gln	
					185					190					195	
	Cys	Arg	Val	Thr	His	Pro	His	Leu	Pro	Arg	Ala	Leu	Met	Arg	Ser	
					200					205					210	
	Thr	Thr	Lys	Thr	Ser	Gly	Pro	Arg	Ala	Ala	Pro	Glu	Val	Tyr	Ala	
					215					220					225	
	Phe	Ala	Thr	Pro	Glu	Trp	Pro	Gly	Ser	Arg	Asp	Lys	Arg	Thr	Leu	
					230					235					240	
25	Ala	Cys	Leu	Ile	Gln	Asn	Phe	Met	Pro	Glu	Asp	Ile	Ser	Val	Gln	
					245					250					255	
	Trp	Leu	His	Asn	Glu	Val	Gln	Leu	Pro	Asp	Ala	Arg	His	Ser	Thr	
					260					265					270	
	Thr	Gln	Pro	Arg	Lys	Thr	Lys	Gly	Ser	Gly	Phe	Phe	Val	Phe	Ser	
					275					280					285	
	Arg	Leu	Glu	Val	Thr	Arg	Ala	Glu	Trp	Gln	Glu	Lys	Asp	Glu	Phe	
					290					295					300	
30	Ile	Cys	Arg	Ala	Val	His	Glu	Ala	Ala	Ser	Pro	Ser	Gln	Thr	Val	
					305					310					315	
	Gln	Arg	Ala	Val	Ser	Val	Asn	Pro	Gly	Lys						
					320					325						

(4) INFORMATION FOR SEQ ID NO:3:

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- ° (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 175
 (B) TYPE: amino acids
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: Unknown
- (ii) MOLECULE TYPE: Polypeptide ϵ -chain of rat IgE

- 5 (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Kindsrogel et al.
 (B) TITLE:
 (C) JOURNAL: DNA
 (D) VOLUME: 1
 (E) ISSUE:
 (F) PAGES: 335-343
 10 (G) DATE: 1982

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:3:

	Asn	Leu	Asn	Ile	Thr	Gln	Gln	Gln	Trp	Met	Ser	Glu	Ser	Thr	Phe	
					5					10					15	
	Thr	Cys	Lys	Val	Thr	Ser	Gln	Gly	Glu	Asn	Tyr	Trp	Ala	His	Thr	
					20					25					30	
15	Arg	Arg	Cys	Ser	Asp	Asp	Glu	Pro	Arg	Gly	Val	Ile	Thr	Tyr	Leu	
					35					40					45	
	Ile	Pro	Pro	Ser	Pro	Leu	Asp	Leu	Tyr	Glu	Asn	Gly	Thr	Pro	Lys	
					50					55					60	
	Leu	Thr	Cys	Leu	Val	Leu	Asp	Leu	Glu	Ser	Glu	Glu	Asn	Ile	Thr	
					65					70					75	
	Val	Thr	Trp	Val	Arg	Glu	Arg	Lys	Lys	Ser	Ile	Gly	Ser	Ala	Ser	
20					80					85					90	
	Gln	Arg	Ser	Thr	Lys	His	His	Asn	Ala	Thr	Thr	Ser	Ile	Thr	Ser	
					95					100					105	
	Ile	Leu	Pro	Val	Asp	Ala	Lys	Asp	Trp	Ile	Glu	Gly	Glu	Gly	Tyr	
					110					115					120	
	Gln	Cys	Arg	Val	Asp	His	Pro	His	Phe	Pro	Lys	Pro	Ile	Val	Arg	
					125					130					135	
25	Ser	Ile	Thr	Lys	Ala	Leu	Gly	Leu	Arg	Ser	Ala	Pro	Glu	Val	Tyr	
					140					145					150	
	Val	Phe	Leu	Pro	Pro	Glu	Glu	Glu	Glu	Lys	Asn	Lys	Arg	Thr	Leu	
					155					160					165	
	Thr	Cys	Leu	Ile	Gln	Asn	Phe	Phe	Pro	Glu						
					170					175						

(5) INFORMATION FOR SEQ ID NO:4:

- 30 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 315
 (B) TYPE: amino acids
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: Unknown

- 35 (ii) MOLECULE TYPE: Polypeptide ϵ -chain of mouse IgE

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° (x) PUBLICATION INFORMATION:
 (A) AUTHORS: Ishida et al.
 (B) TITLE:
 (C) JOURNAL: EMBO
 (D) VOLUME: 1
 (E) ISSUE:
 (F) PAGES: 1117-1123
 5 (G) DATE: 1982

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:4:

	Val	Arg	Pro	Val	Thr	His	Ser	Leu	Ser	Pro	Pro	Trp	Ser	Tyr	Ser	
					5					10					15	
	Ile	His	Arg	Cys	Asp	Pro	Asn	Ala	Phe	His	Ser	Thr	Ile	Gln	Leu	
					20					25					30	
10	Tyr	Cys	Phe	Ile	Tyr	Gly	His	Ile	Leu	Asn	Asp	Val	Ser	Val	Ser	
					35					40					45	
	Trp	Leu	Met	Asp	Asp	Arg	Glu	Ile	Thr	Asp	Thr	Leu	Ala	Gln	Thr	
					50					55					60	
	Val	Leu	Ile	Lys	Glu	Glu	Gly	Lys	Leu	Ala	Ser	Thr	Cys	Ser	Lys	
					65					70					75	
	Leu	Asn	Ile	Thr	Glu	Gln	Gln	Trp	Met	Ser	Glu	Ser	Thr	Phe	Thr	
					80					85					90	
15	Cys	Arg	Val	Thr	Ser	Gln	Gly	Cys	Asp	Tyr	Leu	Ala	His	Thr	Arg	
					95					100					105	
	Arg	Cys	Pro	Asp	His	Glu	Pro	Arg	Gly	Ala	Ile	Thr	Tyr	Leu	Ile	
					110					115					120	
	Pro	Pro	Ser	Pro	Leu	Asp	Leu	Tyr	Gln	Asn	Gly	Ala	Pro	Lys	Leu	
					125					130					135	
	Thr	Cys	Leu	Val	Leu	Asp	Leu	Glu	Ser	Glu	Lys	Asn	Val	Asn	Val	
					140					145					150	
20	Thr	Trp	Asn	Gln	Glu	Lys	Lys	Thr	Ser	Val	Ser	Ala	Ser	Gln	Trp	
					155					160					165	
	Tyr	Thr	Lys	His	His	Asn	Asn	Ala	Thr	Thr	Ser	Ile	Thr	Ser	Ile	
					170					175					180	
	Leu	Pro	Val	Val	Ala	Lys	Asp	Trp	Ile	Glu	Gly	Tyr	Gly	Tyr	Gln	
					185					190					195	
25	Cys	Ile	Val	Asp	Arg	Pro	Asp	Phe	Pro	Lys	Pro	Ile	Val	Arg	Ser	
					200					205					210	
	Ile	Thr	Leu	Pro	Gln	Val	Ser	Gln	Arg	Ser	Ala	Pro	Glu	Val	Tyr	
					215					220					225	
	Val	Phe	Pro	Pro	Pro	Glu	Glu	Glu	Ser	Glu	Asp	Lys	Arg	Thr	Leu	
					230					235					240	
	Thr	Cys	Leu	Ile	Gln	Asn	Phe	Phe	Pro	Glu	Asp	Ile	Ser	Val	Gln	
					245					250					255	
30	Trp	Leu	Gly	Asp	Gly	Lys	Leu	Ile	Ser	Asn	Ser	Gln	His	Ser	Thr	
					260					265					270	
	Thr	Thr	Pro	Leu	Lys	Ser	Asn	Gly	Ser	Asn	Gln	Gly	Phe	Phe	Ile	
					275					280					285	
	Phe	Ser	Arg	Leu	Glu	Val	Ala	Lys	Thr	Leu	Trp	Thr	Gln	Arg	Lys	
					290					295					300	

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Gln Phe Thr Cys Gln Val Ile His Glu Ala Leu Gln Lys Pro Arg
305 310 315

(6) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

5

- (A) LENGTH: 15
(B) TYPE: amino acid
(C) STRANDEDNESS: not applicable
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

10

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp
1 5 10 15

(7) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

15

- (A) LENGTH: 28
(B) TYPE: amino acid
(C) STRANDEDNESS: not applicable
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

20

Lys Lys Leu Arg Arg Leu Leu Tyr Met Ile Tyr Met Ser Gly Leu
1 5 10 15
Ala Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp Tyr
20 25 30

25 (8) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17
(B) TYPE: amino acid
(C) STRANDEDNESS: not applicable
(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Lys Lys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
1 5 10 15
Glu Leu

5 (9) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 22

(B) TYPE: amino acid

(C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Lys Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro
1 5 10 15
Lys Val Ser Ala Ser His Leu
20

15

(10) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

20 (C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

25 Tyr Met Ser Gly Leu Ala Val Arg Val His Val Ser Lys Glu Glu
1 5 10 15

(11) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: amino acid

30 (C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

35

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Tyr Asp Pro Asn Tyr Leu Arg Thr Asp Ser Asp Lys Asp Arg Phe
 1 5 10 15
 Leu Gln Thr Met Val Lys Leu Phe Asn Arg Ile Lys
 20 25

5

(12) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 24

(B) TYPE: amino acid

(C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Gly Ala Tyr Ala Arg Cys Pro Asn Gly Thr Arg Ala Leu Thr Val
 1 5 10 15
 Ala Glu Leu Arg Gly Asn Ala Glu Leu
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15

(13) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 15

(B) TYPE: amino acid

(C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly Val Leu
 1 5 10 15

25

(14) INFORMATION FOR SEQ ID NO:13:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 39

(B) TYPE: amino acids

(C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

30

(ii) MOLECULE TYPE:

(A) DESCRIPTION: peptide

35

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(xi) SEQUENCE DESCRIPTION:SEQ ID NO:13:

Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Gly Pro Gly Lys Thr
 5 10 15
 Lys Gly Ser Gly Phe Phe Val Phe Gly Pro Gly Lys Thr Lys Gly
 20 25 30
 Ser Gly Phe Phe Val Phe Gly Lys Met
 35

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(15) INFORMATION FOR SEQ ID NO:14:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21
 (B) TYPE: amino acids
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: unknown

10

(ii) MOLECULE TYPE:

(A) DESCRIPTION: peptide

(xi) SEQUENCE DESCRIPTION:SEQ ID NO:14:

15

Val Ser Phe Gly Val Trp Ile Arg Thr Pro Pro Ala Tyr Arg Pro
 1 5 10 15
 Pro Asn Ala Pro Ile Leu
 20

(16) INFORMATION FOR SEQ ID NO:15:

20

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 28
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

25

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Lys Lys Lys Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln
 1 5 10 15
 Ser Leu Asp Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

30

(17) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 38
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not applicable

35

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(D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

5 Lys Lys Leu Arg Arg Leu Leu Tyr Met Ile Tyr Met Ser Gly Leu
 1 5 10 15
 Ala Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp Tyr
 20 25 30
 Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 35 40

10 (18) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 25

(B) TYPE: amino acid

(C) STRANDEDNESS: not applicable

(D) TOPOLOGY: unknown

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

Tyr Met Ser Gly Leu Ala Val Arg Val His Val Ser Lys Glu Glu
 1 5 10 15
 Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

(19) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27

(B) TYPE: amino acid

(C) STRANDEDNESS: not applicable

25 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

30 Lys Lys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr
 1 5 10 15
 Glu Leu Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

(20) INFORMATION FOR SEQ ID NO:19:

(i) SEQUENCE CHARACTERISTICS:

35

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- (A) LENGTH: 32
- (B) TYPE: amino acid
- (C) STRANDEDNESS: not applicable
- (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

5 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

Lys	Lys	Phe	Asn	Asn	Phe	Thr	Val	Ser	Phe	Trp	Leu	Arg	Val	Pro
1			5						10					15
Lys	Val	Ser	Ala	Ser	His	Leu	Lys	Thr	Lys	Gly	Ser	Gly	Phe	Phe
			20						25					30
Val	Phe													

10

(21) INFORMATION FOR SEQ ID NO:20:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 37
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not applicable
 - (D) TOPOLOGY: unknown

15

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

Tyr	Asp	Pro	Asn	Tyr	Leu	Arg	Thr	Asp	Ser	Asp	Lys	Asp	Arg	Phe
1			5						10					15
20	Leu	Gln	Thr	Met	Val	Lys	Leu	Phe	Asn	Arg	Ile	Lys	Lys	Thr
			20						25					30
Gly	Ser	Gly	Phe	Phe	Val	Phe								
			35											

(22) INFORMATION FOR SEQ ID NO:21:

25

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 34
 - (B) TYPE: amino acid
 - (C) STRANDEDNESS: not applicable
 - (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

Gly	Ala	Tyr	Ala	Arg	Cys	Pro	Asn	Gly	Thr	Arg	Ala	Leu	Thr	Val
1			5						10					15

35

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° Ala Glu Leu Arg Gly Asn Ala Glu Leu Lys Thr Lys Gly Ser Gly
 20 25 30
 Phe Phe Val Phe

(23) INFORMATION FOR SEQ ID NO:22:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 25
 (B) TYPE: amino acid
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly Val Leu
 1 5 10 15
 Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

15 (24) INFORMATION FOR SEQ ID NO:23:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 26
 (B) TYPE: amino acids
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: unknown

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Gly Pro Gly Lys Thr
 5 10 15
 25 Lys Gly Ser Gly Phe Phe Val Phe Gly Lys Met
 20 25

(25) INFORMATION FOR SEQ ID NO:24:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 6
 (B) TYPE: amino acids
 (C) STRANDEDNESS: not applicable
 (D) TOPOLOGY: unknown

(ii) MOLECULE TYPE: linking group

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° (xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

Pro Pro Xaa Pro Xaa Pro
5

(2) INFORMATION FOR SEQ ID NO:25:

5

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 16 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10 Thr Ala Lys Ser Lys Lys Phe Pro Ser Tyr Thr Ala Thr Tyr Gln Phe
1 5 10 15

(2) INFORMATION FOR SEQ ID NO:26:

15 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

20 Gly Ile Leu Glu Ser Arg Gly Ile Lys Ala Arg Ile Thr His Val Asp
1 5 10 15
Thr Glu Ser Tyr
20

(2) INFORMATION FOR SEQ ID NO:27:

25

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Trp Val Arg Asp Ile Ile Asp Asp Phe Thr Asn Glu Ser Ser Gln Lys
1 5 10 15
Thr

35

(2) INFORMATION FOR SEQ ID NO:28:

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- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 16 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

Asp	Val	Ser	Thr	Ile	Val	Pro	Tyr	Ile	Gly	Pro	Ala	Leu	Asn	His	Val
1				5					10					15	

10 (2) INFORMATION FOR SEQ ID NO:29:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 25 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

15 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

Ala	Leu	Asn	Ile	Trp	Asp	Arg	Phe	Asp	Val	Phe	Cys	Thr	Leu	Gly	Ala
1			5					10						15	
Thr	Thr	Gly	Tyr	Leu	Lys	Gly	Asn	Ser							
			20					25							

20

(2) INFORMATION FOR SEQ ID NO:30:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 23 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

25

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

Asp	Ser	Glu	Thr	Ala	Asp	Asn	Leu	Glu	Lys	Thr	Val	Ala	Ala	Leu	Ser
1				5				10						15	
Ile	Leu	Pro	Gly	Ile	Gly	Cys									
			20												

30

(2) INFORMATION FOR SEQ ID NO:31:

- (i) SEQUENCE CHARACTERISTICS:
 - (A) LENGTH: 39 amino acids
 - (B) TYPE: amino acid
 - (D) TOPOLOGY: linear

35

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

5 Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met Val Ala
 1 5 10 15
 Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe Ala Ala
 20 25 30
 Thr Asn Phe Val Glu Ser Cys
 35

(2) INFORMATION FOR SEQ ID NO:32:

10

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 21 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

15

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

Asp Ile Glu Lys Lys Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe
 1 5 10 15
 Asn Val Val Asn Ser
 20

20 (2) INFORMATION FOR SEQ ID NO:33:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

25 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

Lys Trp Phe Lys Thr Asn Ala Pro Asn Gly Val Asp Glu Lys Ile Arg
 1 5 10 15
 Ile

30 (2) INFORMATION FOR SEQ ID NO:34:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 14 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Leu Gln Gly Lys Ile Ala Asp Ala Val Lys Ala Lys Gly
1 5 10

5 (2) INFORMATION FOR SEQ ID NO:35:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 19 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

10 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

Gly Leu Ala Ala Gly Leu Val Gly Met Ala Ala Asp Ala Met Val Glu
1 5 10 15
Asp Val Asn

15 (2) INFORMATION FOR SEQ ID NO:36:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 20 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Ser Thr Glu Thr Gly Asn Gln His His Tyr Gln Thr Arg Val Val Ser
1 5 10 15
Asn Ala Asn Lys
20

25 (2) INFORMATION FOR SEQ ID NO:37:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 29 amino acids
(B) TYPE: amino acid
(D) TOPOLOGY: linear

30 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

Lys Lys Gln Tyr Ile Lys Ala Asn Ser Lys Phe Ile Gly Ile Thr Glu
1 5 10 15

35

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° Leu Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
20 25

(2) INFORMATION FOR SEQ ID NO:38:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 34 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

10 Lys Lys Phe Asn Asn Phe Thr Val Ser Phe Trp Leu Arg Val Pro Lys
1 5 10 15
Val Ser Ala Ser His Leu Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe
20 25 30
Val Phe

(2) INFORMATION FOR SEQ ID NO:39:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

20 Tyr Met Ser Gly Leu Ala Val Arg Val His Val Ser Lys Glu Glu Gly
1 5 10 15
Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
20 25

25 (2) INFORMATION FOR SEQ ID NO:40:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 32 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

30 Gly Ile Leu Glu Ser Arg Gly Ile Lys Ala Arg Ile Thr His Val Asp
1 5 10 15

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° Thr Glu Ser Tyr Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO:41:

- 5 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 29 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

Trp Val Arg Asp Ile Ile Asp Asp Phe Thr Asn Glu Ser Ser Gln Lys
 1 5 10 15
 Thr Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

15 (2) INFORMATION FOR SEQ ID NO:42:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 28 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

20 (ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

Asp Val Ser Thr Ile Val Pro Tyr Ile Gly Pro Ala Leu Asn His Val
 1 5 10 15
 Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

25

(2) INFORMATION FOR SEQ ID NO:43:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 37 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

30

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Ala Leu Asn Ile Trp Asp Arg Phe Asp Val Phe Cys Thr Leu Gly Ala
 1 5 10 15

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Thr Thr Gly Tyr Leu Lys Gly Asn Ser Gly Gly Lys Thr Lys Gly Ser
 20 25 30
 Gly Phe Phe Val Phe
 35

5 (2) INFORMATION FOR SEQ ID NO:44:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 35 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

10

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

Asp Ser Glu Thr Ala Asp Asn Leu Glu Lys Thr Val Ala Ala Leu Ser
 1 5 10 15
 Ile Leu Pro Gly Ile Gly Cys Gly Gly Lys Thr Lys Gly Ser Gly Phe
 20 25 30
 Phe Val Phe
 35

15

(2) INFORMATION FOR SEQ ID NO:45:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 51 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Glu Glu Ile Val Ala Gln Ser Ile Ala Leu Ser Ser Leu Met Val Ala
 1 5 10 15
 Gln Ala Ile Pro Leu Val Gly Glu Leu Val Asp Ile Gly Phe Ala Ala
 20 25 30
 Thr Asn Phe Val Glu Ser Cys Gly Gly Lys Thr Lys Gly Ser Gly Phe
 35 40 45
 Phe Val Phe
 50

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(2) INFORMATION FOR SEQ ID NO:46:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 33 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

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Asp Ile Glu Lys Lys Ile Ala Lys Met Glu Lys Ala Ser Ser Val Phe
1           5           10           15
5 Asn Val Val Asn Ser Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val
    20           25           30
Phe

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(2) INFORMATION FOR SEQ ID NO:47:

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10 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 29 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

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15 Lys Trp Phe Lys Thr Asn Ala Pro Asn Gly Val Asp Glu Lys Ile Arg
    1           5           10           15
    Ile Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
        20           25

```

(2) INFORMATION FOR SEQ ID NO:48:

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20 (i) SEQUENCE CHARACTERISTICS:
    (A) LENGTH: 26 amino acids
    (B) TYPE: amino acid
    (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

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25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

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Gly Leu Gln Gly Lys Ile Ala Asp Ala Val Lys Ala Lys Gly Gly Gly
1           5           10           15
Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
    20           25

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30 (2) INFORMATION FOR SEQ ID NO:49:

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    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 31 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

Gly Leu Ala Ala Gly Leu Val Gly Met Ala Ala Asp Ala Met Val Glu
 1 5 10 15
 5 Asp Val Asn Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO:50:

(i) SEQUENCE CHARACTERISTICS:

10 (A) LENGTH: 32 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

15 Ser Thr Glu Thr Gly Asn Gln His His Tyr Gln Thr Arg Val Val Ser
 1 5 10 15
 Asn Ala Asn Lys Gly Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25 30

(2) INFORMATION FOR SEQ ID NO:51:

20 (i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

25 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

Phe Phe Leu Leu Thr Arg Ile Leu Thr Ile Pro Gln Ser Leu Asp Gly
 1 5 10 15
 Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

30 (2) INFORMATION FOR SEQ ID NO:52:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

35 (ii) MOLECULE TYPE: peptide

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(xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Leu Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly Val Gly
 1 5 10 15
 Gly Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 20 25

(2) INFORMATION FOR SEQ ID NO:53:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

Lys Lys Leu Arg Arg Leu Leu Tyr Met Ile Tyr Met Ser Gly Leu Ala
 1 5 10 15
 Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp Tyr Gly Gly
 20 25 30
 Lys Thr Lys Gly Ser Gly Phe Phe Val Phe
 35 40

(2) INFORMATION FOR SEQ ID NO:54:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Gly Ala Tyr Ala Arg Cys Pro Asn Gly Thr Arg Ala Leu Thr Val Ala
 1 5 10 15
 Glu Leu Arg Gly Asn Ala Glu Leu Gly Gly Lys Thr Lys Gly Ser Gly
 20 25 30
 Phe Phe Val Phe
 35

(2) INFORMATION FOR SEQ ID NO:55:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 54 amino acids
 (B) TYPE: amino acid

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(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

5 Thr Ala Lys Ser Lys Lys Phe Pro Ser Tyr Thr Ala Thr Tyr Gln Phe
 1 5 10 15
 Gly Gly Gly Ala Tyr Ala Arg Cys Pro Asn Gly Thr Arg Ala Leu Thr
 20 25 30
 Val Ala Glu Leu Arg Gly Asn Ala Glu Leu Gly Gly Lys Thr Lys Gly
 35 40 45
 Ser Gly Phe Phe Val Phe
 50

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(2) INFORMATION FOR SEQ ID NO:56:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 51 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

20 Tyr Asp Pro Asn Tyr Leu Arg Thr Asp Ser Asp Lys Asp Arg Phe Leu
 1 5 10 15
 Gln Thr Met Val Lys Leu Phe Asn Asp Arg Phe Leu Gln Thr Met Val
 20 25 30
 Lys Leu Phe Asn Arg Ile Lys Gly Gly Lys Thr Lys Gly Ser Gly Phe
 35 40 45
 Phe Val Phe
 50

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(2) INFORMATION FOR SEQ ID NO:57:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 27 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

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(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

35 Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Gly Gly Leu Ser Glu Ile
 1 5 10 15
 Lys Gly Val Ile Val His Arg Leu Glu Gly Val
 20 25

35

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(2) INFORMATION FOR SEQ ID NO:58:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 42 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Gly Gly Lys Lys Leu Arg
 1 5 10 15
 10 Arg Leu Leu Tyr Met Ile Tyr Met Ser Gly Leu Ala Val Arg Val His
 20 25 30
 Val His Lys Glu Glu Gln Tyr Tyr Asp Tyr
 35 40

(2) INFORMATION FOR SEQ ID NO:59:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 36 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Gly Gly Gly Ala Tyr Ala
 1 5 10 15
 Arg Cys Pro Asn Glu Thr Arg Ala Leu Thr Val Ala Glu Leu Arg Gly
 20 25 30
 Asn Ala Glu Leu
 35

(2) INFORMATION FOR SEQ ID NO:60:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 52 amino acids

(B) TYPE: amino acid

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

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° Lys Thr Lys Gly Ser Gly Phe Phe Val Phe Gly Gly Tyr Asp Pro
 1 5 10 15
 Asn Tyr Leu Arg Thr Asp Ser Asp Lys Asp Arg Phe Leu Gln Thr Met
 20 25 30
 Val Lys Leu Phe Asn Asp Arg Phe Leu Gln Thr Met Val Lys Leu Phe
 35 40 45
 Asn Arg Ile Lys
 50
 5

(2) INFORMATION FOR SEQ ID NO:61:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 16 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 10

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

Leu Ser Glu Ile Lys Gly Val Ile Val His Arg Leu Glu Gly Val
 1 5 10 15
 15

(2) INFORMATION FOR SEQ ID NO:62:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear
 20

(ii) MOLECULE TYPE: peptide

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

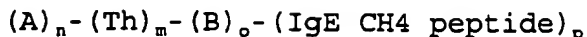
Lys Lys Leu Arg Arg Leu Leu Tyr Met Ile Tyr Met Ser Gly Leu Ala
 1 5 10 15
 25 Val Arg Val His Val Ser Lys Glu Glu Gln Tyr Tyr Asp Tyr Lys Thr
 20 25 30
 Lys Gly Ser Gly Phe Phe Val Phe
 35 40
 30

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° I claim:

1. A peptide immunogen represented by the formula:



wherein: A is an amino acid, α -NH₂, a fatty acid or a derivative thereof, or an invasin;

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B is an amino acid;

Th is a helper T cell epitope, an analog or segment thereof;

10

IgE CH4 peptide is SEQ ID NO:1 or an immunogenic analog thereof;

n is from 1 to 10;

m is from 1 to 4;

o is from 0 to 10; and

p is from 1 to 3.

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2. The peptide immunogen of Claim 1 wherein p is 1.

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3. The peptide immunogen of Claim 1 wherein Th is selected from the group consisting SEQ ID NOS:5-12, 14, 26-36, 61 and an immunogenic analog or segment thereof.

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4. The peptide immunogen of Claim 2 wherein Th is selected from the group consisting SEQ ID NOS:5-12, 14, 26-36, 61 and an immunogenic analog or segment thereof.

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5. The peptide immunogen of Claim 1 selected from the group consisting SEQ ID NOS:13, 15-23, 37-50, 51-56 and 62.

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6. The peptide immunogen of Claims 3 selected from the group consisting SEQ ID NOS:51-56 and 62.

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7. The peptide immunogen of Claim 1 wherein A is a fatty acid.

8. The peptide immunogen of Claim 2 wherein A is a fatty acid.

9. The peptide immunogen of Claim 1 wherein A is a fatty acid derivative.

10. The peptide immunogen of Claim 2 wherein A is a fatty acid derivative.

11. The peptide immunogen of Claim 9 wherein the fatty acid derivative is Pam₃Cys.

12. The peptide immunogen of Claim 10 wherein the fatty acid derivative is Pam₃Cys.

13. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 1 in a pharmaceutically acceptable delivery system.

14. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 2 in a pharmaceutically acceptable delivery system.

15. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 3 in a pharmaceutically acceptable delivery system.

16. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 4 in a pharmaceutically acceptable delivery system.

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17. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 5 in a pharmaceutically acceptable delivery system.
18. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 6 in a pharmaceutically acceptable delivery system.
19. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 7 in a pharmaceutically acceptable delivery system.
20. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 8 in a pharmaceutically acceptable delivery system.
21. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 9 in a pharmaceutically acceptable delivery system.
22. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 10 in a pharmaceutically acceptable delivery system.
23. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 11 in a pharmaceutically acceptable delivery system.
24. A vaccine composition comprising an effective amount of a peptide immunogen of Claim 12 in a pharmaceutically acceptable delivery system.
25. A vaccine composition comprising an effective amount of a mixture of peptide immunogens of Claim 9 in a pharmaceutically acceptable delivery system.

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26. A vaccine composition comprising an effective amount of a mixture of peptide immunogens of Claim 10 in a pharmaceutically acceptable delivery system.

27. A vaccine composition comprising an effective amount of a mixture of peptide immunogens of Claim 11 in a pharmaceutically acceptable delivery system.

28. A vaccine composition comprising an effective amount of a mixture of peptide immunogens of Claim 12 in a pharmaceutically acceptable delivery system.

29. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 13.

30. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 14.

31. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 15.

32. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 16.

33. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 17.

34. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 18.

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35. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 19.

36. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 20.

37. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 21.

38. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 22.

39. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 23.

40. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 24.

41. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 25.

42. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 26.

43. A method of treating allergic reactions by administering an effective amount of a vaccine composition according to Claim 27.

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° 44. A method of treating allergic reactions by
administering an effective amount of a vaccine composition
according to Claim 28.

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INTERNATIONAL SEARCH REPORT

International application No.
PCT/US95/03741

A. CLASSIFICATION OF SUBJECT MATTER

IPC(6) :C07K 19/00, 16/46; A16K 39/395

US CL :424/275.1

According to International Patent Classification (IPC) or to both national classification and IPC

B. FIELDS SEARCHED

Minimum documentation searched (classification system followed by classification symbols)

U.S. : 424/275.1; 530/402, 406, 324

Documentation searched other than minimum documentation to the extent that such documents are included in the fields searched

Electronic data base consulted during the international search (name of data base and, where practicable, search terms used)

APS, Medline, Derwent

search terms allergy, treatment, IgE, anti-IgE

C. DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
X ---- Y	EP, A1 0 403 312 , (STANWORTH ET AL.) 19 December 1990, see claims 1 and 11.	1, 2, 13, 14, 29, 30 ----- 1-44
Y	Molecular Immunology, Volume 30, Number 11, issued 1993, Shaw et al., "Influence of the T-Helper Epitope on the Titre and Affinity of Antibodies to B-Cell Epitopes after Co-immunization", pages 961-968, see table 1.	4, 16, 32
Y	Infection and Immunity, Volume 60, Number 11, issued November 1992, Chong et al., "Identification of T- and B-Cell Epitopes of the S2 and S3 Subunits of Pertussis Toxin by Use of Synthetic Peptides", pages 4640-4647, see abstract and table 1.	3-6,15-18, 31-34



Further documents are listed in the continuation of Box C.



See patent family annex.

* Special categories of cited documents:	*T	later document published after the international filing date or priority date and not in conflict with the application but cited to understand the principle or theory underlying the invention
A document defining the general state of the art which is not considered to be of particular relevance	*X*	document of particular relevance; the claimed invention cannot be considered novel or cannot be considered to involve an inventive step when the document is taken alone
E earlier document published on or after the international filing date	*Y*	document of particular relevance; the claimed invention cannot be considered to involve an inventive step when the document is combined with one or more other such documents, such combination being obvious to a person skilled in the art
L document which may throw doubts on priority claim(s) or which is cited to establish the publication date of another citation or other special reason (as specified)	*Z*	document member of the same patent family
O document referring to an oral disclosure, use, exhibition or other means		
P document published prior to the international filing date but later than the priority date claimed		

Date of the actual completion of the international search

26 MAY 1995

Date of mailing of the international search report

19 JUN 1995

Name and mailing address of the ISA/US
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INTERNATIONAL SEARCH REPORT

 International application No.
 PCT/US95/03741

C (Continuation). DOCUMENTS CONSIDERED TO BE RELEVANT

Category*	Citation of document, with indication, where appropriate, of the relevant passages	Relevant to claim No.
Y	Journal of Experimental Medicine, Volume 172, issued July, 1990, Su et al., "Identification and Characterization of T Helper Cell Epitopes of the Major Outer Membrane Protein of Chlamydia trachomatis", pages 203-212, see abstract and page 208.	3-5, 15-17, 31-33
Y	Journal of Immunology, Volume 152, issued 1994, Reynolds et al., "T and B Epitope Determination and Analysis of Multiple Antigenic Peptides for the Schistosoma mansoni Experimental Vaccine Triose-Phosphate Isomerase", pages 193-200, see figure 2.	3-5, 15-17, 31-33
Y	Nature, Volume 336, Number 22, issued 1988, Sinigaglia et al., "A Malaria T-cell epitope recognised with most mouse and human MHC class II molecules", pages 778-780, see table 2.	3-5, 15-17, 31-33
Y	Vaccine, Volume 11, Number 13, issued 1993, Russell-Jones et al., "Peptide sequences with strong stimulatory activity for lymphoid cells: implications for vaccine development", pages 1310-1315, see table 1.	3-5, 15-17, 31-33
Y	Journal of Immunology, Volume 151, Number 11, issued 1993, Reece et al., "Mapping the Major Human T Helper Epitopes of Tetanus Toxin", pages 6175-6184, see entire document.	3-6, 15-18, 31-34
Y	International Journal of Peptide and Protein Research, Volume 40, issued 1992, Wiesmuller et al., "Solid phase synthesis of lipopeptide vaccines eliciting epitope-specific B-, T-helper and T-killer cell response", pages 255-260, see entire document.	1-44
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